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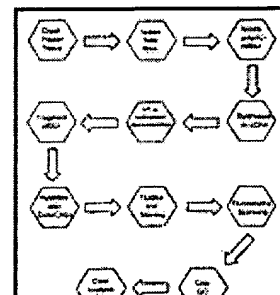
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(54) Title: GENE EXPRESSION PROFILES IN LIVER CANCER

(57) Abstract

The present invention identifies the global changes in gene expression associated with liver cancer by examining gene expression in tissue from normal liver, metastatic malignant liver and hepatocellular carcinoma. The present invention also identifies expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug toxicity, drug efficacy and drug metabolism.



Description Claims

GENE EXPRESSION PROFILES IN LIVER CANCER RELATED APPLICATIONS This application is related to U. S. Provisional Application 60/211,379, filed on June 14,2000, and is related to U. S. Provisional Application 60/237,054, filed October 2,2000, and is related to U. S. Application 09/880,107, filed June 14,2001, each of which is herein incorporated by reference in its entirety.

BACKGROUND OF THE INVENTION Primary hepatocellular carcinoma (HCC) is a widespread cancer throughout the world, especially prevalent where the incidence of chronic hepatitis B (HBV) and hepatitis C (HCV) viral infections are endemic (Groen, (1999) *Semin. Oncol. Nurs.* 15,48-57; Idilman et al., (1998) *J. Viral. Hepat.* 5,110-117; Di Bisceglie et al., (1998) *Hepatol.* 28, 1161-1165; Johnson, (1997) *Hepatogastroenterology*44, 307-312; Sheu, (1997) *J.*

Gastroenterol. Hepatol. 12, S309-313). Hepatocellular carcinomas are very malignant tumors that generally offer a poor prognosis, dependent on the size of the tumor, the effect on normal liver functions, and the involvement of metastases. They are best treated by surgical resection, when the tumors are diagnosed at a stage where this is a viable possibility, but the recurrence rate for these cancers remains high (Johnson, (1997) *Hepatogastroenterology* 44, 307-312; Schafer & Sorrel, (1999) *Lancet* 353,1253-1257; Groen, (1999) *Semin. Oncol. Nurs.* 15,48-57; Sitzman, (1995) *World. J. Surg.* 19,790-794; DiCarlo, (1995) *Hepato-Gastroenterol.* 42,222-259; Tanaka et al., (1996) *Hepato-Gastroenterol.* 43,1172-1181; El-Assal et al., (1997) *Surgery* 122,571-577).

Numerous risk factors for the development of HCC have been identified: cirrhosis, HBV or HCV infection, being male, alcohol-related liver disease, exposure to aflatoxins, vinyl chloride and radioactive thorium dioxide, cigarette smoking, ingestion of inorganic arsenic, the use of oral contraceptives and anabolic steroids, iron accumulation, and various inherited metabolic disorders (hemochromatosis, glycogen storage disease, porphyria, tyrosinemia, oc-I-antitrypsin deficiency) (Di Bisceglie et al., (1998) *Hepatol.* 28,1161-1165; Chen et al., (1997) *J. Gastroenterol. Hepatol.* 12, S294-308 ; Schafer & Sorrell (1999) *Lancet* 353,1253-1257; Groen, (1999) *Semin. Oncol. Nurs.* 15,48-57; Idilman et al., (1998) *J. Viral. Hepat.* 5,110-117; Johnson, (1997) *Hepato-Gastroenterol.* 44,307-312).

In addition to liver tumors attributed to hepatocellular carcinoma, there are liver tumors that arise as metastases from primary tumors in other parts of the body. These tumors most often metastasize from the gastrointestinal organs, primarily the colon and rectum, but it is possible for metastatic liver cancers to occur from primary cancers throughout the body (Sitzman, (1990) *Hepatic Neoplasia*, in Bayless (editor) *Current Therapy in Gastroenterology and Liver Disease*, Marcel Dekker; Groen, (1999) *Semin.*

Oncol. Nurs. 15,48-57). These cancers can be treated using the routine therapies such as chemotherapy, radiotherapy, surgical resection, liver transplantation, chemoembolization, cryosurgery, or a combination of therapies (Sitzman 1990, Groen 1999).

The characterization of genes that are differentially expressed in tumorigenesis is an important step in identifying those that are intimately involved in the details of a cell's transformation from normal to cancerous. Little is known about the molecular changes that take place in the liver during the course of tumor progression. While changes in the expression level of individual genes has been reported, for example, galectin-3 (Hsu et al., (1999) *Int. J. Cancer* 81: 519-526; Iurisci et al., (2000) *Clin. Cancer Res.* 6: 1389-1393; Nakamura et al., (1999) *Int. J. Oncol.* 15: 143-148) and pancreatic secretory trypsin inhibitor (PTSI, Ohmachi et al., (1994) *Int. J. Cancer* 55: 728-734) the investigation of the global changes in gene expression which occur in liver have not been documented. The identification of genes that are expressed in tumor tissue at differing levels, but not expressed at any level in normal liver tissue

will be very valuable for monitoring tumor progression. The identification of genes and ESTs that are expressed in both types of tumors, i. e., primary hepatocellular carcinomas as well as metastatic tumors of a different origin, and not in normal liver cells would be extremely valuable for the diagnosis of liver cancer. Thus there exists a need in the art for the identification of new genes and ESTs to serve as molecular markers to monitor the onset and development of liver cancer. These and other needs are met by the present invention.

SUMMARY OF THE INVENTION The present invention identifies the global changes in gene expression associated with liver cancer by examining gene expression in tissue from normal liver, metastatic malignant liver and hepatocellular carcinoma. The present invention also identifies expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug toxicity, drug efficacy and drug metabolism.

The invention includes methods of diagnosing the presence or absence of liver cancer in a patient comprising the step of detecting the level of expression in a tissue sample of two or more genes from Tables 3-9; wherein differential expression of the genes in Tables 3-9 is indicative of liver cancer. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 3-5. In some preferred embodiments, the method may include detecting the expression level of one or more genes selected from a group consisting Tetraspan NET-6 protein; collagen, type V, alpha; and glypican 3.

The invention also includes methods of detecting the progression of liver cancer and/or differentiating nonmetastatic from metastatic disease. For instance, methods of the invention include detecting the progression of liver cancer in a patient comprising the step of detecting the level of expression in a tissue sample of two or more genes from 3-9; wherein differential expression of the genes in Tables 3-9 is indicative of liver cancer progression. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 3-5.

In some aspects, the present invention provides a method of monitoring the treatment of a patient with liver cancer, comprising administering a pharmaceutical composition to the patient and preparing a gene expression profile from a cell or tissue sample from the patient and comparing the patient gene expression profile to a gene expression from a cell population comprising normal liver cells or to a gene expression profile from a cell population comprising liver cancer cells or to both. In some preferred embodiments, the gene profile will include the expression level of one or more genes in Tables 3-9. In other preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 3-5.

In another aspect, the present invention provides a method of treating a patient with liver cancer, comprising administering to the patient a pharmaceutical composition, wherein the composition alters the expression of at least one gene in Tables 3-9, preparing a gene expression profile from a cell or tissue sample from the patient comprising tumor cells and comparing the patient expression profile to a gene expression profile from an untreated cell population comprising liver cancer cells. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 3-5.

In one aspect, the present invention provides a method of diagnosing hepatocellular carcinoma in a patient, comprising detecting the level of expression in a tissue sample of two or more genes from Tables 3-9, wherein differential expression of the genes in Tables 3-9 is indicative of hepatocellular carcinoma. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 3 or 5.

In another aspect, the present invention provides a method of detecting the progression of hepatocellular carcinoma in a patient, comprising detecting the level of expression in a tissue sample of two or more genes from Tables 3-9; wherein differential expression of the genes in Tables 3-9 is indicative of hepatocellular carcinoma progression.

In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 3 or 5.

The present invention also provides materials and methods for monitoring the treatment of a patient with a hepatocellular carcinoma. The present invention provides a method of monitoring the treatment of a patient with hepatocellular carcinoma, comprising administering a pharmaceutical composition to the patient, preparing a gene expression profile from a cell or tissue sample from the patient and comparing the patient gene expression profile to a gene expression from a cell population comprising normal liver cells or to a gene expression profile from a cell population comprising hepatocellular carcinoma cells or to both. In some preferred embodiments, the method may include detecting the level of expression of one or more genes from the genes listed in Tables 3-9. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 3 or 5.

In a related aspect, the present invention provides a method of treating a patient with hepatocellular carcinoma, comprising administering to the patient a pharmaceutical composition, wherein the composition alters the expression of at least one gene in Tables 3- 9, preparing a gene expression profile from a cell or tissue sample from the patient comprising hepatocellular carcinoma cells and comparing the patient expression profile to a gene expression profile from an untreated cell population comprising hepatocellular carcinoma cells. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 3 or 5.

The present invention provides a method of diagnosing a metastatic liver tumor in a patient, comprising detecting the level of expression in a tissue sample of two or more genes from Tables 3-9, wherein differential expression of the genes in Tables 3-9 is indicative of a metastatic liver tumor. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 4 or 5.

The present invention provides a method of detecting the progression of a metastatic liver tumor in a patient, comprising detecting the level of expression in a tissue sample of two or more genes from Tables 3-9, wherein differential expression of the genes in Tables 3-9 is indicative of a metastatic liver tumor progression. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 4 or 5.

In a related aspect, the present invention provides a method of monitoring the treatment of a patient with a metastatic liver tumor, comprising administering a pharmaceutical composition to the patient, preparing a gene expression profile from a cell or tissue sample from the patient and comparing the patient gene expression profile to a gene expression from a cell population comprising normal liver cells or to a gene expression profile from a cell population comprising metastatic liver tumor cells or to both. In some preferred embodiments, the method of the present invention may include detecting the expression level of one or more genes selected from the genes listed in Tables 3-9. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 4 or 5.

In some preferred embodiments, the present invention provides a method of treating a patient with a metastatic liver tumor, comprising administering to the patient a pharmaceutical composition, wherein

the composition alters the expression of at least one gene in Tables 3-9, preparing a gene expression profile from a cell or tissue sample from the patient comprising metastatic liver tumor cells and comparing the patient expression profile to a gene expression profile from an untreated cell population comprising metastatic liver tumor cells. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 4 or 5.

The invention also includes methods of differentiating metastatic liver cancer from hepatocellular carcinoma in a patient comprising the step of detecting the level of expression in a tissue sample of two or more genes from Tables 3-9; wherein differential expression of the genes in Tables 3-9 is indicative of metastatic liver cancer rather than hepatocellular carcinoma.

The invention further includes methods of screening for an agent capable of modulating the onset or progression of liver cancer, comprising the steps of exposing a cell to the agent; and detecting the expression level of two or more genes from Tables 3-9. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 3-5.

Any of the methods of the invention described above may include the detection of at least 2 genes from the tables. Preferred methods may detect all or nearly all of the genes in the tables. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 3-5.

The invention further includes compositions comprising at least two oligonucleotides, wherein each of the oligonucleotides comprises a sequence that specifically hybridizes to a gene in Tables 3-9 as well as solid supports comprising at least two probes, wherein each of the probes comprises a sequence that specifically hybridizes to a gene in Tables 3-9. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 3-5.

The invention further includes computer systems comprising a database containing information identifying the expression level in liver tissue of a set of genes comprising at least two genes in Tables 3-9; and a user interface to view the information. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 3-5. The database may further include sequence information for the genes, information identifying the expression level for the set of genes in normal liver tissue and malignant tissue (metastatic and nonmetastatic) and may contain links to external databases such as GenBank.

Lastly, the invention includes methods of using the databases, such as methods of using the disclosed computer systems to present information identifying the expression level in a tissue or cell of at least one gene in Tables 3-9, comprising the step of comparing the expression level of at least one gene in Tables 3-9 in the tissue or cell to the level of expression of the gene in the database. In some preferred embodiments, one or more genes may be selected from a group consisting of the genes listed in Tables 3-5.

BRIEF DESCRIPTION OF THE DRAWINGS Figure 1 is a flow chart showing a schematic representation of the experimental protocol.

Figures 2A-2C are graphs of the number of genes present in all samples as a function of the number of samples for the second sample set.

DETAILED DESCRIPTION Many biological functions are accomplished by altering the expression of various genes through transcriptional (e. g., through control of initiation, provision of RNA precursors,

RNA processing, etc.) and/or translational control. For example, fundamental biological processes such as cell cycle, cell differentiation and cell death, are often characterized by the variations in the expression levels of groups of genes.

Changes in gene expression also are associated with pathogenesis. For example, the lack of sufficient expression of functional tumor suppressor genes and/or the over expression of oncogene/protooncogenes could lead to tumorigenesis or hyperplastic growth of cells (Marshall, (1991) *Cell*, 64,313-326; Weinberg, (1991) *Science*, 254,1138-1146).

Thus, changes in the expression levels of particular genes (e. g., oncogenes or tumor suppressors) serve as signposts for the presence and progression of various diseases.

Monitoring changes in gene expression may also provide certain advantages during drug screening development. Often drugs are screened and prescreened for the ability to interact with a major target without regard to other effects the drugs have on cells. Often such other effects cause toxicity in the whole animal, which prevent the development and use of the potential drug.

The present inventors have examined tissue samples from normal liver, metastatic malignant liver and hepatocellular carcinoma to identify the global changes in gene expression associated with liver cancer. The protocol used is schematically represented in Figure 1. These global changes in gene expression, also referred to as expression profiles, provide useful markers for diagnostic uses as well as markers that can be used to monitor disease states, disease progression, drug toxicity, drug efficacy and drug metabolism.

Definitions In the description that follows, numerous terms and phrases known to those skilled in the art are used. In the interests of clarity and consistency of interpretation, the definitions of certain terms and phrases are provided.

The present invention provides compositions and methods to detect the level of expression of genes that may be differentially expressed dependent upon the state of the cell, i. e., normal versus cancerous. As used herein, the phrase "detecting the level of expression" includes methods that quantitate expression levels as well as methods that determine whether a gene of interest is expressed at all. Thus, an assay which provides a yes or no result without necessarily providing quantification of an amount of expression is an assay that requires "detecting the level of expression" as that phrase is used herein.

As used herein, oligonucleotide sequences that are complementary to one or more of the genes described herein, refers to oligonucleotides that are capable of hybridizing under stringent conditions to at least part of the nucleotide sequence of said genes. Such hybridizable oligonucleotides will typically exhibit at least about 75% sequence identity at the nucleotide level to said genes, preferably about 80% or 85% sequence identity or more preferably about 90% or 95% or more sequence identity to said genes.

"Bind (s) substantially" refers to complementary hybridization between a probe nucleic acid and a target nucleic acid and embraces minor mismatches that can be accommodated by reducing the stringency of the hybridization media to achieve the desired detection of the target polynucleotide sequence.

The terms "background" or "background signal intensity" refer to hybridization signals resulting from non-specific binding, or other interactions, between the labeled target nucleic acids and components of the oligonucleotide array (e. g., the oligonucleotide probes, control probes, the array substrate, etc.). Background signals may also be produced by intrinsic fluorescence of the array components themselves. A single background signal can be calculated for the entire array, or a different background signal may

be calculated for each target nucleic acid. In a preferred embodiment, background is calculated as the average hybridization signal intensity for the lowest 5% to 10% of the probes in the array, or, where a different background signal is calculated for each target gene, for the lowest 5% to 10% of the probes for each gene. Of course, one of skill in the art will appreciate that where the probes to a particular gene hybridize well and thus appear to be specifically binding to a target sequence, they should not be used in a background signal calculation.

Alternatively, background may be calculated as the average hybridization signal intensity produced by hybridization to probes that are not complementary to any sequence found in the sample (e. g., probes directed to nucleic acids of the opposite sense or to genes not found in the sample such as bacterial genes where the sample is mammalian nucleic acids).

Background can also be calculated as the average signal intensity produced by regions of the array that lack any probes at all.

The phrase "hybridizing specifically to" refers to the binding, duplexing or hybridizing of a molecule substantially to or only to a particular nucleotide sequence or sequences under stringent conditions when that sequence is present in a complex mixture (e. g., total cellular) DNA or RNA.

The term "mismatch control" or "mismatch probe" refer to a probe whose sequence is deliberately selected not to be perfectly complementary to a particular target sequence.

For each mismatch (MM) control in a high-density array there typically exists a corresponding perfect match (PM) probe that is perfectly complementary to the same particular target sequence. The mismatch may comprise one or more bases.

While the mismatch (s) may be located anywhere in the mismatch probe, terminal mismatches are less desirable as a terminal mismatch is less likely to prevent hybridization of the target sequence. In a particularly preferred embodiment, the mismatch is located at or near the center of the probe such that the mismatch is most likely to destabilize the duplex with the target sequence under the test hybridization conditions.

The term "perfect match probe" refers to a probe that has a sequence that is perfectly complementary to a particular target sequence. The test probe is typically perfectly complementary to a portion (subsequence) of the target sequence. The perfect match (PM) probe can be a "test probe", a "normalization control" probe, an expression level control probe and the like. A perfect match control or perfect match probe is, however, distinguished from a "mismatch control" or "mismatch probe." As used herein a "probe" is defined as a nucleic acid, capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (i. e., A, G, U, C or T) or modified bases (7- deazaguanosine, inosine, etc.). In addition, the bases in probes may be joined by a linkage other than a phosphodiester bond, so long as it does not interfere with hybridization. Thus, probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages.

The term "stringent conditions" refers to conditions under which a probe will hybridize to its target subsequence, but with only insubstantial hybridization to other sequences or to other sequences such that the difference may be identified. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the

specific sequence at a defined ionic strength and pH.

Typically, stringent conditions will be those in which the salt concentration is at least about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (e. g., 10 to 50 nucleotide). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide.

The "percentage of sequence identity" or "sequence identity" is determined by comparing two optimally aligned sequences or subsequences over a comparison window or span, wherein the portion of the polynucleotide sequence in the comparison window may optionally comprise additions or deletions (i. e., gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical monomer unit (e. g., nucleic acid base or amino acid residue) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity. Percentage sequence identity when calculated using the programs GAP or BESTFIT (see below) is calculated using default gap weights.

Homology or identity may be determined by BLAST (Basic Local Alignment Search Tool) analysis using the algorithm employed by the programs blastp, blastn, blastx, tblastn and tblastx (Karin et al., (1990) Proc. Natl. Acad. Sci. USA 87,2264-2268 and Altschul, (1993) J. Mol. Evol. 36,290-300, fully incorporated by reference) which are tailored for sequence similarity searching. The approach used by the BLAST program is to first consider similar segments between a query sequence and a database sequence, then to evaluate the statistical significance of all matches that are identified and finally to summarize only those matches which satisfy a preselected threshold of significance. For a discussion of basic issues in similarity searching of sequence databases, see Altschul et al., (1994) Nature Genet. 6,119-129) which is fully incorporated by reference. The search parameters for histogram, descriptions, alignments, expect (i. e., the statistical significance threshold for reporting matches against database sequences), cutoff, matrix and filter are at the default settings. The default scoring matrix used by blastp, blastx, tblastn, and tblastx is the BLOSUM62 matrix (Henikoff et al., (1992) Proc. Natl. Acad. Sci. USA 89, 10915- 10919, fully incorporated by reference). Four blastn parameters were adjusted as follows: Q=10 (gap creation penalty); R=10 (gap extension penalty); wink=1 (generates word hits at everywinkth position along the query); and gapw=16 (sets the window width within which gapped alignments are generated). The equivalent Blastp parameter settings were Q=9; R=2; wink=1 ; and gapw=32. A Bestfit comparison between sequences, available in the GCG package version 10.0, uses DNA parameters GAP=50 (gap creation penalty) and LEN=3 (gap extension penalty) and the equivalent settings in protein comparisons are GAP=8 and LEN=2.

Uses for the Liver Cancer Markers as Diagnostics As described herein, the genes and gene expression information provided in Tables 3-9 may be used as diagnostic markers for the prediction or identification of the malignant state of the liver tissue. For instance, a liver tissue sample or other sample from a patient may be assayed by any of the methods described herein or by any other method known to those skilled in the art, and the expression levels from a gene or genes from the Tables, in particular the genes in Tables 3-5, may be compared to the expression levels found in normal liver tissue, tissue from metastatic liver cancer or hepatocellular carcinoma tissue.

Expression profiles generated from the tissue or other sample that substantially resemble an expression profile from normal or diseased liver tissue may be used, for instance, to aid in disease diagnosis. Comparison of the expression data, as well as available sequence or other information may be done by researcher or diagnostician or may be done with the aid of a computer and databases as described above.

Use of the Liver Cancer Markers for Monitoring Disease Progression As described above, the genes and gene expression information provided in Tables 3-9 may also be used as markers for the monitoring of disease progression, for instance, the development of liver cancer. For instance, a liver tissue sample or other sample from a patient may be assayed by any of the methods described above, and the expression levels in the sample from a gene or genes from or 3-9 may be compared to the expression levels found in normal liver tissue, tissue from metastatic liver cancer or hepatocellular carcinoma tissue. Comparison of the expression data, as well as available sequence or other information may be done by researcher or diagnostician or may be done with the aid of a computer and databases as described above.

Use of the Liver Cancer Markers for Drug Screening According to the present invention, the genes identified in Tables 3-9 may be used as markers to evaluate the effects of a candidate drug or agent on a cell, particularly a cell undergoing malignant transformation, for instance, a liver cancer cell or tissue sample. A candidate drug or agent can be screened for the ability to stimulate the transcription or expression of a given marker or markers (drug targets) or to down-regulate or counteract the transcription or expression of a marker or markers. According to the present invention, one can also compare the specificity of drugs' effects by looking at the number of markers affected by different drugs and comparing them. More specific drugs will affect fewer transcriptional targets. Similar sets of markers identified for two drugs indicates a similarity of effects.

Agents that are assayed in the above methods can be randomly selected or rationally selected or designed. As used herein, an agent is said to be randomly selected when the agent is chosen randomly without considering the specific sequences involved in the association of the a protein of the invention alone or with its associated substrates, binding partners, etc. An example of randomly selected agents is the use a chemical library or a peptide combinatorial library, or a growth broth of an organism.

As used herein, an agent is said to be rationally selected or designed when the agent is chosen on a nonrandom basis which takes into account the sequence of the target site and/or its conformation in connection with the agents action. Agents can be rationally selected or rationally designed by utilizing the peptide sequences that make up these sites.

For example, a rationally selected peptide agent can be a peptide whose amino acid sequence is identical to or a derivative of any functional consensus site.

The agents of the present invention can be, as examples, peptides, small molecules, vitamin derivatives, as well as carbohydrates. Dominant negative proteins, DNA encoding these proteins, antibodies to these proteins, peptide fragments of these proteins or mimics of these proteins may be introduced into cells to affect function. "Mimic" as used herein refers to the modification of a region or several regions of a peptide molecule to provide a structure chemically different from the parent peptide but topographically and functionally similar to the parent peptide (see Grant, (1995) in Molecular Biology and Biotechnology Meyers (editor) VCH Publishers). A skilled artisan can readily recognize that there is no limit as to the structural nature of the agents of the present invention.

Assay Formats The genes identified as being differentially expressed in liver cancer may be used in a variety of nucleic acid detection assays to detect or quantitate the expression level of a gene or multiple genes in a given sample. Any hybridization assay format may be used, including solution-based and solid support-based assay formats, for example, traditional Northern blotting. Other suitable assay formats that may be used for detecting gene expression levels include, but are not limited to, nuclease protection, RT-PCR and differential display methods. These methods are useful for some embodiments of the invention; however, methods and assays of the invention are most efficiently designed with array or chip hybridization-based methods for detecting the expression of a large number of genes. Assays and methods of the invention may utilize available formats to simultaneously screen at least about 100,

preferably about 1000, more preferably about 10,000 and most preferably about 1,000,000 or more different nucleic acid hybridizations.

Assays to monitor the expression of a marker or markers as defined in Tables 3-9 may utilize any available means of monitoring for changes in the expression level of the nucleic acids of the invention. As used herein, an agent is said to modulate the expression of a nucleic acid of the invention if it is capable of up-or down-regulating expression of the nucleic acid in a cell.

In one assay format, gene chips containing probes to at least two genes from Tables 3-9 may be used to directly monitor or detect changes in gene expression in the treated or exposed cell as described in more detail above. In another format, cell lines that contain reporter gene fusions between the open reading frame and/or the 3' or 5' regulatory regions of a gene in Tables 3-9 and any assayable fusion partner may be prepared. Numerous assayable fusion partners are known and readily available including the firefly luciferase gene and the gene encoding chloramphenicol acetyltransferase (Alam et al., (1990) Anal.

Biochem. 188, 245-254). Cell lines containing the reporter gene fusions are then exposed to the agent to be tested under appropriate conditions and time. Differential expression of the reporter gene between samples exposed to the agent and control samples identifies agents which modulate the expression of the nucleic acid.

Additional assay formats may be used to monitor the ability of the agent to modulate the expression of one or more genes identified in Tables 3-9. For instance, as described above, mRNA expression may be monitored directly by hybridization of probes to the nucleic acids of the invention. Cell lines are exposed to the agent to be tested under appropriate conditions and time and total RNA or mRNA is isolated by standard procedures such those disclosed in Sambrook et al., (1989) Molecular Cloning-A Laboratory Manual, Cold Spring Harbor Laboratory Press).

In another assay format, cells or cell lines are first identified which express the gene products of the invention physiologically. Cell and/or cell lines so identified would be expected to comprise the necessary cellular machinery such that the fidelity of modulation of the transcriptional apparatus is maintained with regard to exogenous contact of agent with appropriate surface transduction mechanisms and/or the cytosolic cascades. Such cell lines may be, but are not required to be, derived from liver tissue. Further, such cells or cell lines may be transduced or transfected with an expression vehicle (e. g., a plasmid or viral vector) construct comprising an operable non-translated 5'-promoter containing end of the structural gene encoding the instant gene products fused to one or more antigenic fragments, which are peculiar to the instant gene products, wherein said fragments are under the transcriptional control of said promoter and are expressed as polypeptides whose molecular weight can be distinguished from the naturally occurring polypeptides or may further comprise an immunologically distinct tag. Such a process is well known in the art (see Sambrook et al., (1989) Molecular Cloning-A Laboratory Manual, Cold Spring Harbor Laboratory Press).

Cells or cell lines transduced or transfected as outlined above are then contacted with agents under appropriate conditions; for example, the agent comprises a pharmaceutically acceptable excipient and is contacted with cells comprised in an aqueous physiological buffer such as phosphate buffered saline (PBS) at physiological pH, Eagles balanced salt solution (BSS) at physiological pH, PBS or BSS comprising serum or conditioned media comprising PBS or BSS and serum incubated at 37°C. Said conditions may be modulated as deemed necessary by one of skill in the art. Subsequent to contacting the cells with the agent, said cells will be disrupted and the polypeptides of the lysate are fractionated such that a polypeptide fraction is pooled and contacted with an antibody to be further processed by immunological assay (e. g., ELISA, immunoprecipitation or Western blot). The pool of proteins isolated from the "agent-contacted" sample will be compared with a control sample where only the

excipient is contacted with the cells and an increase or decrease in the immunologically generated signal from the "agent-contacted" sample compared to the control will be used to distinguish the effectiveness of the agent.

Another embodiment of the present invention provides methods for identifying agents that modulate the levels, concentration or at least one activity of a protein (s) encoded by the genes in Tables 3-9. Such methods or assays may utilize any means of monitoring or detecting the desired activity.

In one format, the relative amounts of a protein of the invention between a cell population that has been exposed to the agent to be tested compared to an un-exposed control cell population may be assayed. In this format, probes such as specific antibodies are used to monitor the differential expression of the protein in the different cell populations. Cell lines or populations are exposed to the agent to be tested under appropriate conditions and time. Cellular lysates may be prepared from the exposed cell line or population and a control, unexposed cell line or population. The cellular lysates are then analyzed with the probe, such as a specific antibody.

The genes which are assayed according to the present invention are typically in the form of mRNA or reverse transcribed mRNA. The genes may be cloned or not and the genes may be amplified or not. The cloning itself does not appear to bias the representation of genes within a population. However, it may be preferable to use polyA⁺ RNA as a source, as it can be used with less processing steps.

The sequences of the expression marker genes are in the public databases. Tables 3- 9 provide the Affymetrix gene ID and GenBank accession number for each marker identified. The nucleotide sequence for each marker has been provided in electronic format with this application and these sequences are incorporated herein by reference as are equivalent and related sequences present in the public databases.

Probes based on the sequences of the genes described herein may be prepared by any commonly available method. Oligonucleotide probes for assaying the tissue or cell sample are preferably of sufficient length to specifically hybridize only to appropriate, complementary genes or transcripts. Typically the oligonucleotide probes will be at least 10, 12, 14, 16, 18, 20 or 25 nucleotides in length. In some cases longer probes of at least 30, 40, or 50 nucleotides will be desirable.

Probe design One of skill in the art will appreciate that an enormous number of array designs are suitable for the practice of this invention. The high density array will typically include a number of probes that specifically hybridize to the sequences of interest. See WO 99/32660 for methods of producing probes for a given gene or genes. In addition, in a preferred embodiment, the array will include one or more control probes.

High density array chips of the invention include "test probes." Test probes may be oligonucleotides that range from about 5 to about 500 or about 5 to about 50 nucleotides, more preferably from about 10 to about 40 nucleotides and most preferably from about 15 to about 40 nucleotides in length. In other particularly preferred embodiments the probes are about 20 or 25 nucleotides in length. In another preferred embodiment, test probes are double or single strand DNA sequences. DNA sequences are isolated or cloned from natural sources or amplified from natural sources using natural nucleic acid as templates.

These probes have sequences complementary to particular subsequences of the genes whose expression they are designed to detect. Thus, the test probes are capable of specifically hybridizing to the target nucleic acid they are to detect.

In addition to test probes that bind the target nucleic acid (s) of interest, the high density array can contain a number of control probes. The control probes fall into three categories referred to herein as (1) normalization controls; (2) expression level controls; and (3) mismatch controls.

Normalization controls are oligonucleotide or other nucleic acid probes that are complementary to labeled reference oligonucleotides or other nucleic acid sequences that are added to the nucleic acid sample. The signals obtained from the normalization controls after hybridization provide a control for variations in hybridization conditions, label intensity, "reading" efficiency and other factors that may cause the signal of a perfect hybridization to vary between arrays. In a preferred embodiment, signals (e. g., fluorescence intensity) read from all other probes in the array are divided by the signal (e. g., fluorescence intensity) from the control probes thereby normalizing the measurements.

Virtually any probe may serve as a normalization control. However, it is recognized that hybridization efficiency varies with base composition and probe length. Preferred normalization probes are selected to reflect the average length of the other probes present in the array, however, they can be selected to cover a range of lengths. The normalization control (s) can also be selected to reflect the (average) base composition of the other probes in the array, however in a preferred embodiment, only one or a few probes are used and they are selected such that they hybridize well (i. e., no secondary structure) and do not match any target-specific probes.

Expression level controls are probes that hybridize specifically with constitutively expressed genes in the biological sample. Virtually any constitutively expressed gene provides a suitable target for expression level controls. Typical expression level control probes have sequences complementary to subsequences of constitutively expressed "housekeeping genes" including, but not limited to the P-actin gene, the transferrin receptor gene, the GAPDH gene, and the like.

Mismatch controls may also be provided for the probes to the target genes, for expression level controls or for normalization controls. Mismatch controls are oligonucleotide probes or other nucleic acid probes identical to their corresponding test or control probes except for the presence of one or more mismatched bases. A mismatched base is a base selected so that it is not complementary to the corresponding base in the target sequence to which the probe would otherwise specifically hybridize. One or more mismatches are selected such that under appropriate hybridization conditions (e. g., stringent conditions) the test or control probe would be expected to hybridize with its target sequence, but the mismatch probe would not hybridize (or would hybridize to a significantly lesser extent). Preferred mismatch probes contain a central mismatch. Thus, for example, where a probe is a twenty-mer, a corresponding mismatch probe will have the identical sequence except for a single base mismatch (e. g., substituting a G, a C or a T for an A) at any of positions 6 through 14 (the central mismatch).

Mismatch probes thus provide a control for non-specific binding or cross hybridization to a nucleic acid in the sample other than the target to which the probe is directed. Mismatch probes also indicate whether a hybridization is specific or not. For example, if the target is present the perfect match probes should be consistently brighter than the mismatch probes. In addition, if all central mismatches are present, the mismatch probes can be used to detect a mutation. The difference in intensity between the perfect match and the mismatch probe (I (PM)-I (MM)) provides a good measure of the concentration of the hybridized material.

Nucleic Acid Samples As is apparent to one of ordinary skill in the art, nucleic acid samples used in the methods and assays of the invention may be prepared by any available method or process.

Methods of isolating total mRNA are also well known to those of skill in the art. For example, methods

of isolation and purification of nucleic acids are described in detail in Chapter 3 of Laboratory Techniques in Biochemistry and Molecular Biology: Hybridization With Nucleic Acid Probes, Part I Theory and Nucleic Acid Preparation, Tijssen, (1993) (editor) Elsevier Press. Such samples include RNA samples, but also include cDNA synthesized from a mRNA sample isolated from a cell or tissue of interest. Such samples also include DNA amplified from the cDNA, and an RNA transcribed from the amplified DNA. One of skill in the art would appreciate that it is desirable to inhibit or destroy RNase present in homogenates before homogenates can be used.

Biological samples may be of any biological tissue or fluid or cells from any organism as well as cells raised in vitro, such as cell lines and tissue culture cells.

Frequently the sample will be a "clinical sample" which is a sample derived from a patient.

Typical clinical samples include, but are not limited to, sputum, blood, blood-cells (e. g., white cells), tissue or fine needle biopsy samples, urine, peritoneal fluid, and pleural fluid, or cells therefrom.

Biological samples may also include sections of tissues, such as frozen sections or formalin fixed sections taken for histological purposes.

Solid Supports Solid supports containing oligonucleotide probes for differentially expressed genes of the invention can be filters, polyvinyl chloride dishes, silicon or glass based chips, etc.

Such wafers and hybridization methods are widely available, for example, those disclosed by Beattie (WO 95/11755). Any solid surface to which oligonucleotides can be bound, either directly or indirectly, either covalently or non-covalently, can be used. A preferred solid support is a high density array or DNA chip. These contain a particular oligonucleotide probe in a predetermined location on the array. Each predetermined location may contain more than one molecule of the probe, but each molecule within the predetermined location has an identical sequence. Such predetermined locations are termed features. There may be, for example, about 2,10,100,1000 to 10,000; 100,000 or 400,000 of such features on a single solid support. The solid support, or the area within which the probes are attached may be on the order of a square centimeter.

Oligonucleotide probe arrays for expression monitoring can be made and used according to any techniques known in the art (see for example, Lockhart et al., (1996) Nat.

Biotechnol. 14,1675-1680; McGall et al., (1996) Proc. Nat. Acad. Sci. USA 93,13555- 13460). Such probe arrays may contain at least two or more oligonucleotides that are complementary to or hybridize to two or more of the genes described herein. Such arrays may also contain oligonucleotides that are complementary or hybridize to at least about 2,3, 4,5,6,7,8,9,10,20,30,50,70,100 or or more the genes described herein.

Methods of forming high density arrays of oligonucleotides with a minimal number of synthetic steps are known. The oligonucleotide analogue array can be synthesized on a solid substrate by a variety of methods, including, but not limited to, light-directed chemical coupling, and mechanically directed coupling (see Pirrung et al., (1992) U. S. Patent No.

5,143,854; Fodor et al., (1998) U. S. Patent No. 5,800,992; Chee et al., (1998) 5,837,832.

In brief, the light-directed combinatorial synthesis of oligonucleotide arrays on a glass surface proceeds using automated phosphoramidite chemistry and chip masking techniques. In one specific

implementation, a glass surface is derivatized with a silane reagent containing a functional group, e. g., a hydroxyl or amine group blocked by a photolabile protecting group. Photolysis through a photolithographic mask is used selectively to expose functional groups which are then ready to react with incoming 5' photoprotected nucleoside phosphoramidites. The phosphoramidites react only with those sites which are illuminated (and thus exposed by removal of the photolabile blocking group). Thus, the phosphoramidites only add to those areas selectively exposed from the preceding step. These steps are repeated until the desired array of sequences have been synthesized on the solid surface. Combinatorial synthesis of different oligonucleotide analogues at different locations on the array is determined by the pattern of illumination during synthesis and the order of addition of coupling reagents.

In addition to the foregoing, additional methods which can be used to generate an array of oligonucleotides on a single substrate are described in Fodor et al., (1993). WO 93/09668. High density nucleic acid arrays can also be fabricated by depositing premade or natural nucleic acids in predetermined positions. Synthesized or natural nucleic acids are deposited on specific locations of a substrate by light directed targeting and oligonucleotide directed targeting. Another embodiment uses a dispenser that moves from region to region to deposit nucleic acids in specific spots.

Hybridization Nucleic acid hybridization simply involves contacting a probe and target nucleic acid under conditions where the probe and its complementary target can form stable hybrid duplexes through complementary base pairing (see Lockhart et al., (1999) WO 99/32660).

The nucleic acids that do not form hybrid duplexes are then washed away leaving the hybridized nucleic acids to be detected, typically through detection of an attached detectable label. It is generally recognized that nucleic acids are denatured by increasing the temperature or decreasing the salt concentration of the buffer containing the nucleic acids.

Under low stringency conditions (e. g., low temperature and/or high salt) hybrid duplexes (e. g., DNA-DNA, RNA-RNA or RNA-DNA) will form even where the annealed sequences are not perfectly complementary.

Thus specificity of hybridization is reduced at lower stringency. Conversely, at higher stringency (e. g., higher temperature or lower salt) successful hybridization requires fewer mismatches. One of skill in the art will appreciate that hybridization conditions may be selected to provide any degree of stringency. In a preferred embodiment, hybridization is performed at low stringency, in this case in 6x SSPE-T at 37°C (0.005% Triton x-100) to ensure hybridization and then subsequent washes are performed at higher stringency (e. g., 1 x SSPE-T at 37°C) to eliminate mismatched hybrid duplexes. Successive washes may be performed at increasingly higher stringency (e. g., down to as low as 0.25x SSPET at 37°C to 50°C) until a desired level of hybridization specificity is obtained. Stringency can also be increased by addition of agents such as formamide. Hybridization specificity may be evaluated by comparison of hybridization to the test probes with hybridization to the various controls that can be present (e. g., expression level control, normalization control, mismatch controls, etc.).

In general, there is a tradeoff between hybridization specificity (stringency) and signal intensity. Thus, in a preferred embodiment, the wash is performed at the highest stringency that produces consistent results and that provides a signal intensity greater than approximately 10% of the background intensity. Thus, in a preferred embodiment, the hybridized array may be washed at successively higher stringency solutions and read between each wash. Analysis of the data sets thus produced will reveal a wash stringency above which the hybridization pattern is not appreciably altered and which provides adequate signal for the particular oligonucleotide probes of interest.

Signal Detection The hybridized nucleic acids are typically detected by detecting one or more labels attached to the sample nucleic acids. The labels may be incorporated by any of a number of means well known to those of skill in the art (see Lockhart et al., (1999) WO 99/32660).

Databases The present invention includes relational databases containing sequence information, for instance for the genes of Tables 3-9, as well as gene expression information in various liver tissue samples. Databases may also contain information associated with a given sequence or tissue sample such as descriptive information about the gene associated with the sequence information, or descriptive information concerning the clinical status of the tissue sample, or the patient from which the sample was derived. The database may be designed to include different parts, for instance a sequences database and a gene expression database.

Methods for the configuration and construction of such databases are widely available, for instance, see Akerblom et al., (1999) U. S. Patent 5,953,727, which is herein incorporated by reference in its entirety.

The databases of the invention may be linked to an outside or external database. In a preferred embodiment, as described in Tables 3-9, the external database is GenBank and the associated databases maintained by the National Center for Biotechnology Information (NCBI).

Any appropriate computer platform may be used to perform the necessary comparisons between sequence information, gene expression information and any other information in the database or provided as an input. For example, a large number of computer workstations are available from a variety of manufacturers, such as those available from Silicon Graphics. Client-server environments, database servers and networks are also widely available and appropriate platforms for the databases of the invention.

The databases of the invention may be used to produce, among other things, electronic Northern blots to allow the user to determine the cell type or tissue in which a given gene is expressed and to allow determination of the abundance or expression level of a given gene in a particular tissue or cell.

The databases of the invention may also be used to present information identifying the expression level in a tissue or cell of a set of genes comprising at least one gene in Tables 3-9 comprising the step of comparing the expression level of at least one gene in Tables 3-9 in the tissue to the level of expression of the gene in the database. Such methods may be used to predict the physiological state of a given tissue by comparing the level of expression of a gene or genes in Tables 3-9 from a sample to the expression levels found in tissue from normal liver, malignant liver or hepatocellular carcinoma. Such methods may also be used in the drug or agent screening assays as described below.

Without further description, it is believed that one of ordinary skill in the art can, using the preceding description and the following illustrative examples, make and utilize the compounds of the present invention and practice the claimed methods. The following working examples therefore, specifically point out the preferred embodiments of the present invention, and are not to be construed as limiting in any way the remainder of the disclosure.

EXAMPLES Example 1: Tissue Sample Acquisition and Preparation Figure 1 outlines the experimental protocol used. Liver tissue samples were excised and snap frozen in liquid nitrogen. The clinical data for each of the samples included in this study are outlined in Table 1. The sample set was composed of eight samples of normal liver tissue (N1-N8), five samples of metastatic adenocarcinoma arising from rectum (designated M1 and M3) and colon (M2, M4 and M5) tissues and six samples of primary hepatocellular carcinomas. Samples were named according to type of tissue: HCC=hepatocellular carcinoma,

M=metastatic, N=normal. Table 1 includes the TNM classification (the American Joint Committee on Cancer's system of classifying cancers) of the tissues used as samples where T refers to the extent of the primary tumor, N refers to the absence or presence and extent of regional lymph node metastasis, and M refers to the absence or presence of distant metastasis. Numbers following T, N, and M refer to the size of the primary tumor and the amount of vascular invasion, where 0=no evidence of tumor, lymph node involvement or metastasis, 4=multiple tumors involved, and x=cannot be assessed. Histopathologic grade (Table 1) is a qualitative assessment of differentiation of a tumor, where G1=most differentiated and G4=undifferentiated. Clinical stage (Table 1) characterizes the anatomic extent of disease in the patient from whom the sample was taken, where I and II are early stages, in and IV are late stages.

With minor modifications, the sample preparation protocol followed the Affymetrix GeneChip Expression Analysis Manual. Frozen tissue was first ground to powder using the Spex Certiprep 6800 Freezer Mill. Total RNA was then extracted using Trizol (Life Technologies). The total RNA yield for each sample (average tissue weight of 300 mg) was 200-500 μ g. Next, mRNA was isolated using the Oligotex mRNA Midi kit (Qiagen). Since the mRNA was eluted in a final volume of 400 μ l, an ethanol precipitation step was required to bring the concentration to 1 μ g/ μ l. Using 1-5 μ g of mRNA, double stranded cDNA was created using the SuperScript Choice system (Gibco-BRL). First strand cDNA synthesis was primed with a T7- (dT24) oligonucleotide. The cDNA was then phenol-chloroform extracted and ethanol precipitated to a final concentration of 1 μ g/ μ l. From 2 μ g of cDNA, cRNA was synthesized according to standard procedures. To biotin label the cRNA, nucleotides Bio-11-CTP and Bio-16-UTP (Enzo Diagnostics) were added to the reaction. After a 37°C incubation for six hours, the labeled cRNA was cleaned up according to the Rneasy Mini kit protocol (Qiagen). The cRNA was then fragmented (5x fragmentation buffer: 200 mM Tris-Acetate (pH 8.1), 500 mM KOAc, 150 mM MgOAc) for thirty-five minutes at 94°C.

55 μ g of fragmented cRNA was hybridized on the human Hu35k set and the HuGeneFL array for twenty-four hours at 60 rpm in a 45°C hybridization oven. The chips were washed and stained with Streptavidin Phycoerythrin (SAPE) (Molecular Probes) in Affymetrix fluidics stations. To amplify staining, SAPE solution was added twice with an anti-streptavidin biotinylated antibody (Vector Laboratories) staining step in between.

Hybridization to the probe arrays was detected by fluorometric scanning (Hewlett Packard Gene Array Scanner). Following hybridization and scanning, the microarray images were analyzed for quality control, looking for major chip defects or abnormalities in hybridization signal. After all chips passed QC, the data was analyzed using Affymetrix GeneChip software (v3.0), and Experimental Data Mining Tool (EDMT) software (v1. 0).

Example 2: Gene Expression Analysis All samples were prepared as described and hybridized onto the Affymetrix HuGeneFL array and the Human Hu35k set of arrays. Each chip contains 16-20 oligonucleotide probe pairs per gene or cDNA clone. These probe pairs include perfectly matched sets and mismatched sets, both of which are necessary for the calculation of the average difference. The average difference is a measure of the intensity difference for each probe pair, calculated by subtracting the intensity of the mismatch from the intensity of the perfect match. This takes into consideration variability in hybridization among probe pairs and other hybridization artifacts that could affect the fluorescence intensities. Using the average difference value that has been calculated, the GeneChip software then makes an absolute call for each gene or EST.

The absolute call of present, absent or marginal is used to generate a Gene Signature, a tool used to identify those genes that are commonly present or commonly absent in a given sample set, according to the absolute call. For each set of samples, a median average difference was figured using the average differences of each individual sample within the set. The median average difference must be greater than

150 to assure that the expression level is well above the background noise of the hybridization. For the purposes of this study, only the genes and ESTs with a median average difference greater than 150 have been further studied in detail.

The Gene Signature for one set of samples is compared to the Gene Signature of another set of samples to determine the Gene Signature Differential. This comparison identifies the genes that are consistently present in one set of samples and consistently absent in the second set of samples.

The Gene Signature Curve is a graphic view of the number of genes consistently present in a given set of samples as the sample size increases, taking into account the genes commonly expressed among a particular set of samples, and discounting those genes whose expression is variable among those samples. The curve is also indicative of the number of samples necessary to generate an accurate Gene Signature. As the sample number increases, the number of genes common to the sample set decreases. The curve is generated using the positive Gene Signatures of the samples in question, determined by adding one sample at a time to the Gene Signature, beginning with the sample with the smallest number of present genes and adding samples in ascending order. The curve displays the sample size required for the most consistency and the least amount of expression variability from sample to sample. The point where this curve begins to level off represents the minimum number of samples required for the Gene Signature. Graphed on the x-axis is the number of samples in the set, and on the y-axis is the number of genes in the positive Gene Signature.

Example 3: Gene Expression Analysis of Normal Liver Tissue The gene expression patterns and Gene Signature were individually determined for each sample set: eight samples with normal liver pathology, six samples whose pathology indicated the primary malignancy to be hepatocellular carcinoma, and five samples whose primary colorectal adenocarcinoma had metastasized to the liver. The Gene Signatures obtained for the normal sample set is shown in Figure 2A, the metastatic liver cancer set in Figure 2B and the hepatocellular carcinoma set in Figure 2C.

The Gene Signature considers the present and absent genes alone, and does not take into consideration those that have been called marginal. Table 2 shows the numbers of present genes, called the positive Gene Signature, and the number of absent genes, called the negative Gene Signature, for each of the three sets of samples.

The Gene Signature is the set of genes that are commonly present or commonly absent in N-1 samples of a given sample set. The positive Gene Signature for the normal liver tissues contains 6,213 genes and ESTs. This same set of normal samples did not show any detectable level of expression of 24,900 genes. Many of the genes and ESTs in this positive Gene Signature are housekeeping genes or structural genes that are not only expressed in the liver, but are ubiquitously expressed in tissues throughout the body. Within this positive Gene Signature are also those genes whose expression is specifically restricted to normal liver tissue and those genes required for the liver to function at its normal capacities. It is the group of genes unique to the liver whose expression levels are most likely to change during tumorigenesis. Whether up-regulated or down-regulated or turned completely on or turned completely off, the changes in expression of these vital genes very likely contributes to the drastic changes in liver function caused by the transformation of normal liver cells into cancerous cells.

Example 4: Gene Expression Analysis of Malignant Liver Tissue There are 8, 479 genes and ESTs in the positive Gene Signature for the HCC tumors, and a total of 23,233 genes and ESTs are included in the negative Gene Signature of the HCC samples. This negative Gene Signature includes all the genes that have been completely turned off during tumorigenesis, as well as those genes that are not usually expressed in liver tissue. These results include a number of genes and ESTs that are not regularly expressed in liver tissues, but through the process of tumor production, their expression patterns have

been dramatically altered from no detectable level of expression to some significant level of expression in comparison with the normal liver.

The colorectal metastases in the liver commonly express 5,102 genes and ESTs, and do not show expression of 30,455 additional genes and ESTs. As with the negative Gene Signature for the HCC sample set, the genes included in this data set are generally not expressed in liver tissue, whether tumor or normal tissue. The 5,102 in the sample set of metastatic tumors also identify those genes with expression levels that have been changed from off to on as a result of tumor formation.

Example 5: Analysis of Gene Expression Profiles A differential comparison of the genes and ESTs expressed in the normals and the two different types of liver tumors identifies a subset of the genes included in the positive Gene Signatures that are uniquely expressed in each sample set. This Gene Signature Differential highlights genes whose expression profiles have most dramatically changed in the transformation from normal to diseased liver cells. The parameters for these analyses were set to accommodate variation in expression of one of eight normal samples and one of the six HCC samples or one of the 5 metastatic tumor samples, such that the genes categorized as unique to normal were called present by the software in seven of eight (87%) normal liver samples and were also called absent in five of six HCC (83%) or four of five (80%) metastatic liver tumor. Conversely, the genes categorized as unique to each set of tumors as compared to the normal livers were called present in five of six HCC (83%) or four of five (80%) metastatic tumor samples and absent in seven of eight normal livers (87%).

The Gene Signature Differential comparing the normal livers to those with metastatic tumors identified a total of 903 sequences expressed only in normal liver tissue.

The number of genes or ESTs that meet the median average difference minimum of 150 is 449, of which 289 are genes and the number of ESTs is 160. The remaining ESTs and genes may be indistinguishable from the background noise of the hybridization. The same comparison of normals versus metastatic tumors demonstrates that in the metastatic tumor samples there are 296 uniquely expressed sequences. Those that meet the median average difference minimum requirement are 83 genes and 72 ESTs. Those genes and ESTs expressed in metastatic and not in normal liver tissue are shown in Table 9A and those present in normal liver tissue and not metastatic tissue Table 9B. Numerous genes with differing expression levels in metastatic liver tumor tissue compared to normal tissue were identified. The fifteen genes whose expression level was most different in metastatic as compared to normal tissue are shown in Table 4. Those with the most increased expression are in Table 4A and those with the most decreased expression are in Table 4B. Expression levels were determined by comparing the mean expression values of individual genes in tumor and normal liver samples. Fold change was calculated as a ratio with a p value given as a measure of statistical significance. Fold change is considered significant for a given gene or EST when it is greater than 3.0 with a p value <0.05. Only the characterized genes have been listed; the ESTs with similar fold changes are not presented here. Asterisk (*) in Table 4 denotes those genes that were also identified in the Gene Signature differential between metastatic liver carcinoma and normal liver tissue. A complete listing of all the genes and ESTs with at least a three-fold change in expression is shown in Table 6. Table 6A contains those genes and ESTs whose expression level increased in metastatic tissue relative to normal tissue and Table 6B contains those genes and ESTs whose expression level decreased.

The Gene Signature Differential between the normal liver samples and the HCC samples identifies a total of 47 unique expressers in the normals, 23 with an median average difference of 150,13 of which are named gene and 10 of which are ESTs. When comparing the expression of the HCC samples with the normal livers, there are 243 genes and ESTs only expressed in the HCC samples.

Those genes and ESTs expressed in HCC and not in normal liver tissue are shown in Table 8A and those

present in normal liver tissue and not HCC tissue in Table 8B.

Numerous genes with differing expression levels in HCC compared to normal tissue were identified. The fifteen genes whose expression level was most different in HCC as compared to normal tissue are shown in Table 3. Those with the most increased expression are in Table 3A and those with the most decreased expression are in Table 3B. Expression levels were determined by comparing the mean expression values of individual genes in tumor and normal liver samples. Fold change was calculated as a ratio with a p value given as a measure of statistical significance. Fold change is considered significant for a given gene or EST when it is greater than 3.0 with a p value <0.05 . Only the characterized genes have been listed; the ESTs with similar fold changes are not presented here. Asterisk (*) denotes those genes that were also identified in the Gene Signature differential between hepatocellular carcinoma and normal liver tissue. A complete listing of all the genes and ESTs with at least a three-fold change in expression is shown in Table 7. Table 7A contains those genes and ESTs whose expression level increased in hepatocellular carcinoma tissue relative to normal tissue and Table 7B contains those genes and ESTs whose expression level decreased.

Analysis of sample set identified 24 ESTs and 42 genes that are expressed in both metastatic liver tumors and hepatocellular carcinomas, but not in normal liver tissues. The fifteen genes with the most increase in expression level in both types of cancer are shown in Table 5. Expression levels were determined by comparing the mean expression values of individual genes in tumor and normal liver samples. The mean expression value for HCC and metastatic carcinomas was greater than 250, and included only those genes that showed a fold change greater than 3 with significant p values for both sets of tumors. No detectable level of expression was found in the normal liver tissues for these genes. Only the characterized genes have been listed; the ESTs with similar fold changes that are unique to the tumors are not presented here.

Differential gene expression patterns between normal liver samples and hepatocellular carcinomas and between normal livers and metastatic liver tumors were examined. Genes uniquely expressed by each of the groups individually were identified, as well as those genes that are commonly expressed among liver tumors, whether primary hepatocellular carcinomas or metastatic liver tumors.

Example 6: Association of Liver Cancer with Specific Gene Expression The present inventors have closely examined a number of the tumor-expressing genes to determine if their expression patterns correlate with previous reports published in the literature, and to define a logical relationship between the gene and hepatocarcinogenesis. A number of genes that have previously been associated with either liver cancer or other types of cancers were identified, as well as numerous genes that have not been linked to cancers in any previous studies.

842 genes and ESTs that are up-regulated in hepatocellular carcinomas were identified when compared with normal liver tissue. One such gene is PTTG1, pituitary tumor-transforming gene 1, or securin, an oncogene that inhibits sister chromatid separation during anaphase. Normal tissues show little or no PTTG1 expression, but high levels of expression have been associated with various tumors, including liver tumors, and carcinoma cell lines. Overexpression in NIH3T3 cells resulted in transformation, and these cells caused the formation of tumors when injected into mice. The mechanism by which this tumorigenic activity takes place is postulated to be through the missegregation of sister chromatids, resulting in aneuploidy and, therefore, genetic instability. Our data further support this overexpression of PTTG1 in hepatocellular carcinoma, with a fold change of 10.7 ($P=0.00052$), and no detectable level of expression in normal tissues, as identified by the differential comparison of the consensus patterns of gene expression of these two sample sets.

Galectin 3, LGALS3, one of a family of beta-galactoside-binding animal lectins, is significantly

overexpressed both in primary hepatocellular carcinoma and metastatic liver carcinomas with fold changes of 6.8 ($P=0.00103$) and 27.1 ($P=0.00001$), respectively.

Expression of LGALS3 has been associated with tumor growth, progression, and metastasis, as well as cell-cell and cell-matrix interactions and inflammatory processes. Although expression studies by Hsu et al. revealed no detectable level of galectin-3 in normal liver cells, samples from patients with hepatocellular carcinoma revealed considerable levels of LGALS3 expression. The abnormal expression of this lectin may be an early event in the process of transformation of normal cells to tumor cells, or it may impart an increased capacity for these tumor cells to survive and proliferate. Consistent with the reports by Iurisci et al and Nakamura et al, an increased expression level was found in both types of tumor, but higher concentrations of galectin-3 were observed in liver metastases from colorectal tumors than in the primary HCC tumors.

Another gene that is overexpressed in both hepatocellular carcinoma and metastatic colorectal adenocarcinomas with fold changes of 12.2 ($P=0.00169$) and 58.0 ($P=0.00063$), respectively, is solute carrier family 2, member 3, or glucose transporter 3 (GLUT3). It is one of a family of transmembrane proteins that function as facilitative glucose transporters, which has a unique specificity for brain and neuronal tissues. Glucose uptake and metabolism are known to be increased in carcinoma cells compared to normal cells.

Glucose transporter expression may be elevated in response to the increase in glucose utilization seen in actively proliferating cells, like those of tumors. Conversely, the high levels of glucose transporter expression may be responsible for the enhanced influx of glucose into the tumor cells. Various reports have indicated increased expression of one or more of the family of glucose transporters in malignancies, including those of the brain, esophagus, colon, pancreas, liver, breast, lung, bladder, ovary, testis, skin, head and neck, kidney, and gastric tumors. Kurata et al. (Jpn J Cancer Res 1999 Nov; 90 (11) : 1238-43) specifically report that metastatic liver carcinomas have even higher levels of GLUT3 expression than primary tumors. Consistent with previous studies, the current data confirm the significant overexpression of GLUT3 both in primary liver cancer, hepatocellular carcinoma, and in tumors that have metastasized from the colon and rectum.

One of the significantly underexpressed genes identified by comparing the expression profiles of hepatocellular carcinomas and metastatic liver tumors with that of normal liver tissue is metallothionein 1L. The expression level in HCC is 26.9 fold lower than that of normal ($P=0.00999$), and in metastatic colorectal adenocarcinomas it is down-regulated 66.5 fold ($P=0.00415$). Metallothioneins are heavy metal binding proteins that are involved in detoxification of metals, zinc and copper metabolism cellular adaptation mechanisms, and may be involved in regulating apoptosis. Colorectal adenocarcinoma that has metastasized to the liver has been specifically reported to express less metallothionein than normal liver tissue. Comparison of the consensus patterns of gene expression between metastatic liver samples and normal liver samples show no significant level of MT1L expression in the tumors. Furthermore, additional work has determined that human hepatocellular carcinomas contain much lower levels of metallothioneins than normal liver tissue, and that this decrease correlates with the degree of differentiation and concentrations of copper and zinc in the cells. By comparing the expression profiles of hepatocellular carcinoma and normal liver tissue, this significant reduction in MT1L expression in HCC was confirmed.

A number of enzymes belonging to the family of cytochrome P450s are drastically underexpressed in the two sets of liver tumors in comparison with the normal liver tissue.

For example, expression of CYP2A6 is decreased in HCC with a fold change of 14.2 ($P=0.0307$), and in metastatic tumors with a fold change of 69.9 ($P=0$). CYP8B1 is down-regulated 19.3 fold ($P=0.00807$)

in HCC and 65.1 fold ($P=0.0039$) in liver metastases. In addition to these commonly down-regulated cytochrome P450s, in HCC samples CYP2B is underexpressed 17.9 fold ($P=0.01469$), and in the metastatic liver tumors CYP2C9 and CYP2A7 are underexpressed 84.7 fold ($P=0.00327$) and 72.0 fold ($P=0$), respectively.

Several of these genes are also identified by the differential comparison between expression profiles of tumor and normal, confirming the significant decrease in expression in tumor tissues. Many of these P450 enzymes are critical players in the metabolism of carcinogens, drugs, and other chemical compounds, that are expressed in normal liver.

In addition to genes that are underexpressed in metastatic adenocarcinomas in the liver, more than 1000 genes and ESTs that are overexpressed specifically in these tumors were identified. Two of the most highly up-regulated are claudin 4, also known as clostridium perfringens enterotoxin receptor 1 (fold change 84.4, $P=0$) and occludin (fold change 43.1, $P=0$). Both of these genes are tight junction proteins, responsible for the formation and maintenance of continuous seals around epithelial cells to form a physical barrier that blocks the free passage of water and solutes through the paracellular space.

More specifically, claudin-4 is one member of a family of transmembrane proteins that comprise tight junction strands, and occludin is a cell adhesion molecule (Morita et al., (1999) *Proc. Natl. Acad. Sci. U. S. A.* 96: 511-516). Claudins likely function as paracellular channels, regulating the flow of ions and solutes into and out of the paracellular space (Simon et al., (1999) *Science* 235: 103-106; Wong & Goodenough (1999) *Science* 285: 62; Anderson & Van Itallie (1999) *Curr. Biol.* 9: R922-924). Tight junction proteins also contribute to the regulation of the cellular processes of cell growth and differentiation (Matter & Balda (1999) *Int. Rev. Cytol.* 186: 117-146). Permeability of tight junctions has been associated with tumor formation, where a breakdown in the barrier function of tight junctions allows an increase in the cellular permeability. This breakdown then opens the tight junction barrier, permitting invasion by tumor cells (Zak et al., (2000) *Pflugers Arch.*

440: 179-183; Mullin (1997) *J. Exp. Zool.* 279: 484-489). It has been reported that tight junctions of colon tumors leak more than do the tight junctions of normal colon (Soler et al., (1999) *Carcinogenesis* 20: 1425-1431). A complete loss of tight junction function and a loss of cell-cell contact growth control was seen in cells that had been transfected with oncogenic Raf-1, and expression levels of occludin and another claudin are lower in these cells (Li & Morsny (2000) *J. Cell Biol.* 148: 791-800). Occludin expression has been up-regulated in vitro by the addition of various fatty acids that have anti-cancer effects, decreasing the paracellular permeability (Jiang et al., (1998) *Biochem. Biophys. Res.*

Commun. 244: 414-420). The extreme down-regulation of occludin and claudin-4 in metastatic liver tumors is strongly supported by the reports of tight junction breakdown in tumor tissues.

The present study identified 93 significantly up-regulated genes in both primary HCC and metastatic liver tumors that were not found to have any detectable level of expression in the normal samples. Serine protease inhibitor, Kazal type I (SPINK1), also called pancreatic secretory trypsin inhibitor (PSTI) or tumor-associated trypsin inhibitor (TATI), is one such gene. It is highly expressed in the cells of normal pancreas and in the mucosa of the gastrointestinal tract where it offers protection from proteolytic breakdown.

A marked increase in expression is seen in various pancreatic diseases and in tumors of different tissues, including gastric carcinomas, colorectal cancers, and other neoplastic tissues. This increase is presumably due to the elevated expression of trypsin in the tumors, and not related to amplification or rearrangements within the gene. SPINK1 is also considered a valuable marker for a number of solid

tumors. A drastic elevation of SPEK1 in the blood of patients with hepatocellular carcinoma has been seen (see Ohmachi et al.).

Furthermore, it has been suggested that the level of expression correlates with the extent of tumor, such that this heightened expression level could be indicative of HCC under certain conditions. In keeping with this report of overexpression in these tumors, the present expression data show the levels of expression of this gene in HCC samples to be 28.9 times higher than normal ($P=0.00003$), and in metastatic liver tumors the expression level is 9.8 times higher than normal ($P=0.03697$).

Midkine is one of a family of heparin-binding growth factors, inducible by retinoic acid, and is actively involved in cell-cell interactions and angiogenesis. The expression pattern of midkine is highly restricted in normal adult tissues, and no expression has been reported in normal adult liver, although its expression is required during embryogenesis for normal development. However, it is expressed in moderate to high levels in many tumors, including Wilm's tumors of the kidney, stomach, colon, pancreas, lung, esophagus, breast, and liver tumors. The present data confirm these reports, showing a significant overexpression of midkine in hepatocellular carcinoma samples (fold change 9.9, $P=0.02104$) and in liver metastases (fold change 10.4, $P=0.01818$), but no noticeable expression in normal liver.

Stathmin, leukemia-associated phosphoprotein 18, is a phosphoprotein whose expression pattern and phosphorylation status are controlled by extracellular signals responsible for the regulation of the processes of cell proliferation and differentiation. It is also involved in the regulation of cell division via the destabilization of microtubules.

When comparing expression levels between non-malignant tissues and malignant tissues, the tumors generally show a significant up-regulation of this phosphoprotein, specifically lymphomas, leukemias, breast and prostate tumors. One reason proposed for this elevated expression in cancer cells is the dissimilarity in the rates of cell proliferation and states of differentiation between normal and tumor cells. In both HCC samples and metastatic adenocarcinomas, significant up-regulation of stathmin, 9.4 fold in HCC ($P=0.00015$) and 4.8 fold in metastatic tumors ($P=0.00514$) was seen.

Both the genes and ESTs described here will provide valuable information for the identification of new drug targets against liver carcinomas, and that information may be extended for use in the study of carcinogenesis in other tissues.

Although the present invention has been described in detail with reference to examples above, it is understood that various modifications can be made without departing from the spirit of the invention. Accordingly, the invention is limited only by the following claims. All cited patents, applications and publications referred to in this application are herein incorporated by reference in their entirety.

Table 1. Clinical Information for Hepatocellular Carcinoma, Metastatic Liver Tumor, and Normal Liver Samples Included in this Study

Sample	Pathology	Primary Tumor	Age	Gender	Race	TNM
H1	Hepatocellular Carcinoma	Liver	64	Male	Caucasian	T3, Nx, Mx G2 stage III
H2	Hepatocellular Carcinoma	Liver	27	Female	Caucasian	T3, No, Mx G1 stage III
H3	Hepatocellular Carcinoma	Liver	78	Female	Caucasian	T4, Nx, Mx G2 stage III
H4	Hepatocellular Carcinoma	Liver	43	Male	Asioan	T4, N1, Mx G2 stage IV
H5	Hepatocellular Carcinoma	Liver	51	Male	Caucasian	T4, No, Mx G2 stage IV
H6	Hepatocellular Carcinoma	Liver	57	Male	Caucasian	unavailable G2 stage III
M1	Metastatic Adenocarcinoma	Rectum	61	Female	Caucasian	Tx, Nx, M1 G3 stage IV; Duke D
M2	Metastatic Adenocarcinoma	Colon	54	Male	Caucasian	unavailable G2 stage IV; Duke D
M3	Metastatic Adenocarcinoma	Rectum	50	Female		

Caucasian Tx,Nx,M1 G2 stage IV; Duke D M4 Metastatic Adenocarcinoma Colon 60 Male Caucasian Tx,Nx,M1 G2 stage IV; Duke D M5 Metastatic Adenocarcinoma Colon 57 Male Caucasian Tx,Nx,M1 G2 stage IV; Duke D N1 Normal liver 54 Female Caucasian N2 Normal liver 55 Female Caucasian N3 Normal liver 58 Male Caucasian N4 Normal liver 44 Female Caucasian N5 Normal liver 40 Female Caucasian N6 Normal liver 72 Female Caucasian N7 Normal liver 48 Female Unknown N8 Normal liver 55 Female Caucasian Table 2. Summary of genes and ESTs Expressed in HCC, Metastatic Liver Tumors, and Normal Livers Hepatocellular Colorectal Normal Livers Carcinoma Metastases I. Fingerprint of Gene Expression Genes and ESTs commonly expressed in sample set 8479 5102 6213 Genes and ESTs commonly unexpressed in sample set 23233 30455 24900 II. Fold Change Genes and ESTs overexpressed in tumors (fold change >3 and p<0.05) 842 1044 Number of Genes 430 603 Number of ESTs 412 441 Genes and ESTs underexpressed in tumors (fold change >3 and p<0.05) 393 1867 Number of Genes 235 1016 Number of ESTs 158 851 III. Differential Comparison between Normal and Tumor Expression Genes and ESTs turned ON in tumors 243 296 Genes and ESTs with expression level above threshold in tumor 77 155 Number of Genes 38 83 Number of ESTs 39 72 Genes and ESTs turned OFF in tumors 47 903 Genes and ESTs with expression level above threshold in normal 23 449 Number of Genes 13 289 Number of ESTs 10 160 Table 3A. Top fifteen genes overexpressed in hepatocellular carcinoma.
 <P>Genbank Seq ID Unigene Cluster Gene Name Fold Change Pvalue
 AA055896 135 Hs.146428 collagen, type V, alpha 1 10.9* 0.000907
 AA156187 339 Hs.81634 ATP synthase, H⁺ transporting, mitochondrial F0 complex, subunit b, isoform 1 9.4 0.02007
 AA428172 986 Hs.8546 Notch (Drosophila) homolog 3 9.6* 0.00195
 AA430032 1009 Hs.252587 pituitary tumor-transforming 1 10.7* 0.00052
 AA505133 1417 Hs.279905 solute carrier family 2 (facilitated glucose transporter), member 3 12.2 0.00169
 AA610116 1499 Hs.102737 tetraspan NET-6 protein 16.4 0.00249
 AA620881 1510 Hs.21858 trinucleotide repeat containing 3 9.5 0.00062
 D31094 1639 Hs.109798 G8 protein 9.4 0.0048
 D51276 1678 Hs.81915 leukemia-associated phosphoprotein p18 (stathmin) 9.4 0.00015
 J03464 2094 Hs.179573 collagen, type I, alpha 2 10.4 0.00979
 M94250 2426 Hs.82045 midkine (neurite growth-promoting factor 2) 9.9* 0.02104
 N33920 2493 Hs.44532 diubiquitin 50.3 0
 W45320 3523 Hs.228059 KRAB-associated protein 1 10.1* 0.00002
 Y00705 3850 Hs.181286 serine protease inhibitor, Kazal type 1 28.9 0.00003
 Z37987 3882 Hs.119651 glypican 3 10.7 0.02304 Table 3B. Top fifteen genes underexpressed in hepatocellular carcinoma.
 <P>Genbank Seq ID Unigene Cluster Gene Name Fold Change Pvalue
 AA007395 17 Hs.1219 alcohol dehydrogenase 4 (class II), pi polypeptide 37.8 0.00939
 AA010605 26 Hs.2899 4-hydroxyphenylpyruvate dioxygenase 25.5 0.00855
 AA448002 1113 Hs.23759 putative type II membrane protein 14.1* 0
 H58692 1960 Hs.9520 formyltetrahydrofolate dehydrogenase 20.2 0.00485
 H80901 2005 Hs.272576 ficolin (collagen/fibrinogen domain-containing) 3 (Hakata antigen) 18.6 0
 H81070 2006 Hs.8765 RNA helicase-related protein 39.6 0.00002
 K03192 2127 Hs/183584 cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 6 14.2 0.0307
 M29873 2318 Hs.1360 cytochrome P450, subfamily IIB (phenobarbital-inducible) 17.9 0.01469
 N80129 2703 Hs.94360 metallothionein 1L 26.9 0.00999
 R97419 3004 Hs.35718 cytochrome P450, subfamily VIIIB (sterol 12-alpha-hydroxylase), polypeptide 1 19.3 0.00807
 T48075 3130 Hs.251577 hemoglobin, alpha 1 35.8 0.00471
 T67931 3184 Hs.7645 fibrinogen, B beta polypeptide 17.3 0.00128
 T95813 3262 Hs.137476 KIAA1051 protein 20.4 0.01361
 U56814 3393 Hs.88646 deoxyribonuclease I-like 3 17.7 0.00007
 W88946 3639 Hs.18508 putative glycine-N-acyltransferase 25.3 0.00221 Table 4A. Top fifteen genes overexpressed in metastatic carcinomas of the liver.
 <P>Genbank Seq ID Unigene Cluster Gene Name Fold Change Pvalue
 AA100719 212 Hs.73848 Carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific 50.9* 0.00081
 cross reacting antigen)
 AA156243 340 Hs.154737 Serine protease, umbilical endothelium 41.4* 0.00139
 AA335191 741 Hs.173724 Creatine kinase, brain 47.4* 0.00419
 AA421562 934 Hs.91011 Anterior gradient 2 (Xenopus leavis) homolog 56.3* 0.0041
 AA427468 973 Hs.5372 Claudin 4 84.4* 0
 AA429009 994 Hs.233950 Serine protease inhibitor, Kunitz type 1 30.0* 0.00001
 AA610116

1499 Hs.102737 Tetraspan NET-6 protein 33.7 0.00171
 H58873 1961 Hs.169902 Solute carrier family 2 (facilitated glucose transporter), member 3 58.0* 0.00063
 H94471 2042 Hs.171952 Occludin 43.1 0
 H95233 2048 Hs.31439 Serine protease inhibitor, Kunitz type, 2 47.1 0
 HG2788-HT2896 Hs.27258 Calcyclin binding protein 33.2 0
 M29540 2317 Hs.220529 Carcinoembryonic antigen-related cell adhesion molecule 5 36.6* 0.0116
 M35252 2343 Hs.84072 Transmembrane 4 superfamily member 3 39.1 0
 N92934 2725 Hs.17409 Cysteine-rich protein 1 (intestinal) 35.5 0.002
 X93036 3830 Hs.92323 FXYD domain-containing ion transport regulator 3 42.4* 0.00167 Table 4B. Top fifteen genes underexpressed in metastatic carcinoma of the liver.
 <P>Genbank Seq ID Unigene Cluster Gene Name Fold Change Pvalue
 AA256367 579 Hs.107966 Paraoxonase 3 70.3 0.00192
 H58692 1960 Hs.9520 Formyltetrahydrofolate dehydrogenase 81.4* 0
 K03192 2127 Hs.183584 Cytochrome P450, subfamily IIA(phenobarbital-inducible), polypeptide 6 69.9* 0
 L16883 2166 Hs.167529 Cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 9 84.7 0.00327
 M15656 2268 Hs.234234 Aldolase B, fructose-bisphosphate 96.7* 0
 M16594 2272 Hs.89552 glutathione S-transferase A2 73.2* 0
 M81349 2405 Hs.1955 Serum amyloid A4, constitutive 76.2 0.00015
 N53031 2556 Hs.89691 UDP glycosyltransferase 2 family, polypeptide B4 97.6 0.00022
 N54417 2567 Hs.90765 Fibrinogen, A alpha polypeptide 99.3 0.00001
 R43174 2848 Hs.1898 Paraoxonase 1 74.0* 0.00038
 R49459 2882 Hs.63758 Transferrin receptor 2 85.6 0.00048
 T48039 3129 Hs.2351 Protein C (inactivator of coagulation factors Va and VIIIa) 84.4 0.00112
 T59148 3158 Hs.50966 Carbamoyl-phosphate synthetase 1, mitochondrial 88.9* 0
 U22029 3327 Hs.250615 Cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 7 72.0* 0
 X55283 3734 Hs.1259 Asialoglycoprotein receptor 2 85 0.00084 Table 5. Top fifteen genes expressed in both hepatocellular carcinomas and metastatic liver tumors ad not in normal livers.
 <P>Genbank Seq ID Unigene Cluster Gene Name HCC Fold HCC p Metastatics Metastatic
 Change value Fold p value
 Change
 AA055896 135 Hs.146428 collagen, type V, alpha 1 10.9 0.00907 18.2 0.00146
 AA204927 425 Hs.77899 tropomyosin 1 (alpha) 6.1 0.0014 7.1 0.00074
 AA335191 741 Hs.173724 creatine kinase, brain 6.5 0.01462 47.4 0.00419
 AA429472 997 Hs.236522 DKFZP434P106 protein 8.8 0.00063 8.3 0.00208
 AA434418 1036 Hs.72172 KIAA1115 protein 6.8 0.0032 5.1 0.00498
 AA452724 1149 Hs.166468 programmed cell death 5 7.7 0.00085 7.2 0.00908
 AA610116 1499 Hs.102737 tetraspan NET-6 protein 16.4 0.00249 33.7 0.00171
 AA620881 1510 Hs.21858 trinucleotide repeat containing 3 9.5 0.00062 8.7 0.00735
 D26129 1635 Hs.78224 ribonuclease, RNase A family, 1 (pancreatic) 6.9 0.00008 5.7 0.03827
 D31094 1639 Hs.109798 G8 protein 9.4 0.0048 4.4 0.04845
 D51276 1678 Hs.81915 leukemia-associated phosphoprotein p18 (stathmin) 9.4 0.00015 4.8 0.00514
 H27188 1908 Hs.9930 collagen-binding protein 2 (collagen 2) 5.8 0.01826 4.2 0.02073
 J03464 2094 Hs.179573 collagen, type I, alpha 2 10.4 0.00979 9.8 0.00028
 M94250 2426 Hs.82045 midkine (neurite growth-promoting factor 2) 9.9 0.02104 10.4 0.01818
 Y00705 3850 Hs.181286 serine protease inhibitor, Kazal type 1 28.9 0.0003 9.8 0.03697 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_AA001409_i_at AA001409 1 EST 3.35 up 0.04092
 rc_AA001504_f_at AA001504 2 EST 9.98 up 0.00336
 rc_AA007158_f_at AA007158 15 EST 3.05 up 0.01964
 rc_AA007160_at AA007160 16 EST 6 up 0.01035
 rc_AA010065_s_at AA010065 22 CDC28 protein kinase 2 6.25 up 0.02752
 rc_AA011134_at AA011134 29 EST 28.79 up 0.00602
 rc_AA011383_at AA011383 31 EST 5.17 up 0.00008
 rc_AA025166_s_at AA025166 50 fusion, derived from t (12;16) malignant liposarcoma 3.71 up 0.0052
 rc_AA025277_at AA025277 51 EST 4.56 up 0.03136
 rc_AA026030_at AA026030 53 EST 11.01 up 0.01649
 rc_AA026092_at AA026092 54 EST 3.83 up 0.04596
 rc_AA026150_at AA026150 55 EST 5.14 up 0.01072
 rc_AA026356_at AA026356 57 EST 4.1 up 0.00133
 rc_AA027946_at AA027946 60 EST 3.22 up 0.00098
 rc_AA028103_at AA028103 61 EST 3.52 up 0.01142
 rc_AA028132_s_at AA028132 62 EST 6.25 up 0.00646
 rc_AA029215_at AA029215 64 adaptor-related protein complex 2, beta 1 subunit 3.65 up 0.00037
 rc_AA029356_at AA029356 66 EST 3.68 up

0.01545
 rc_AA033790_f_at AA033790 74 apolipoprotein D 4.21 up 0.03247

 rc_AA034378_f_at AA034378 77 endogenous retroviral protease 4.01 up 0.00974

 rc_AA034499_s_at AA034499 78 zinc finger protein 198 3.7 up 0.02143
 rc_AA040465_at
 AA040465 95 EST 3.25 up 0.00146
 rc_AA043959_at AA043959 101 tropomyosin 4 8.54 up
 0.00222
 rc_AA053007_f_at AA053007 123 putative receptor protein 6.76 up 0.00061

 rc_AA053033_at AA053033 124 EST 7.83 up 0.00379
 rc_AA053102_s_at AA053102 125
 cadherin 17, LI cadherin (liver-intestine) 26.63 up 0.01745
 rc_AA053248_i_at AA053248 126
 EST 7.01 up 0.00003
 rc_AA053248_f_at AA053248 126 EST 6.16 up 0.00191

 rc_AA053424_at AA053424 127 EST 8.76 up 0.01775
 rc_AA053660_at AA053660 128 EST
 15.98 up 0.00003
 rc_AA055805_s_at AA055805 132 EST 42.83 up 0.00142 Table 6A. Genes up
 regulated in metastatic tissue versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known
 Gene Name Fold Change Direction Pvalue
 rc_AA055811_s_at AA055811 133 glycoprotein A33
 (transmembrane) 6.86 up 0.02152
 rc_AA055896_at AA055896 135 collagen, type V, alpha 1
 18.16 up 0.00146
 AA056361_at AA056361 140 integral membrane protein 2C 3.53 up
 0.02983
 rc_AA062721_at AA062721 146 nuclear factor (erythroid-derived 2)-like 1 6.2 up
 0.00024
 rc_AA070206_at AA070206 155 EST 4.26 up 0.00018
 rc_AA070827_at
 AA070827 157 EST 4.41 up 0.01902
 rc_AA074514_at AA074514 160 EST 7.69 up 0

 rc_AA075299_at AA075299 164 EST 34.27 up 0.00002
 rc_AA075580_f_at AA075580 165 EST
 4.98 up 0.02083
 rc_AA075722_at AA075722 166 nuclear transport factor 2 (placental protein 15)
 4.14 up 0.00374
 AA078862_s_at AA078862 173 EST 6.52 up 0.00025
 rc_AA084901_at
 AA084901 181 ribosomal protein S6 kinase, 70kD, polypeptide 2 9.13 up 0.00003

 rc_AA084921_f_at AA084921 182 ribosomal protein S10 3.29 up 0.04872
 kangai 1 (suppression
 of tumorigenicity 6, prostate; CD82
 antigen (R2 leukocyte antigen, antigen detected by
 monoclonal
 rc_AA086232_f_at AA086232 186 and antibody 1A4)) 5.14 up 0.01916

 AA093497_s_at AA093497 199 DEK oncogene (DNA binding) 5.6 up 0.02551
 AA094517_at
 AA094517 202 EST 3.52 up 0.04805
 AA094752_at AA094752 203 hypothetical 43.2 Kd protein
 4.47 up 0.00243
 rc_AA099404_s_at AA099404 208 EST 29.07 up 0
 carcinoembryonic
 antigen-related cell adhesion molecule 6 (non
 rc_AA100719_s_at AA100719 212 specific cross
 reacting antigen) 50.88 up 0.00081
 rc_AA101551_at AA101551 216 EST 24.78 up 0

 rc_AA113149_s_at AA113149 226 tumor suppressing subtransferable candidate 3 10.58 up
 0.00543
 rc_AA113303_at AA113303 227 transmembrane 4 superfamily member (tetraspan NET-
 7) 3.73 up 0.00084
 rc_AA116036_at AA116036 233 chromosome 20 open reading frame 1 8.81
 up 0.00133
 rc_AA121315_at AA121315 237 KIAA1077 protein 4.86 up 0.02438

 rc_AA122386_at AA122386 239 collagen, type V, alpha 2 4.28 up 0.005
 rc_AA126044_at
 AA126044 245 EST 11.23 up 0.00041
 rc_AA126429_at AA126429 247 peroxisomal farnesylated
 protein 3.23 up 0.00478 Table 6A. Genes up regulated in metastatic tissue versus normal sample set
 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue

 rc_AA126459_s_at AA126459 248 DKFZP566B023 protein 3.69 up 0.00352
 rc_AA126719_at
 AA126719 250 EST 5.31 up 0.00026
 AA127712_at AA127712 255 EST 6.59 up 0.03706

 rc_AA127851_at AA127851 257 EST 3.23 up 0.01943
 rc_AA128407_at AA128407 259 EST
 3.78 up 0.01081
 rc_AA128561_at AA128561 261 collagen, type XVII, alpha 1 6.09 up
 0.0433
 rc_AA131084_at AA131084 265 procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3 4.74
 up 0.00427
 rc_AA131162_s_at AA131162 266 EST 4.68 up 0.00042
 rc_AA131584_at
 AA131584 268 DKFZP564O0463 protein 6.83 up 0.00025
 rc_AA131894_at AA131894 269 EST
 3.76 up 0.00384
 rc_AA131919_at AA131919 270 putative type II membrane protein 15.36 up
 0.00027
 rc_AA132032_s_at AA132032 271 trinucleotide repeat containing 1 4.19 up
 0.00295
 rc_AA132554_at AA132554 273 EST 4.96 up 0.02076
 rc_AA132983_at
 AA132983 274 DKFZP586G1517 protein 3.31 up 0.01155
 rc_AA132986_at AA132986 275 EST
 9.47 up 0.00552
 rc_AA133590_at AA133590 282 EST 3.23 up 0.03565
 rc_AA133936_at
 AA133936 284 EST 9.19 up 0.00088
 rc_AA134052_s_at AA134052 285 Rab
 geranylgeranyltransferase, alpha subunit 3.54 up 0.03062
 rc_AA134158_s_at AA134158 287 EST

3.42 up 0.0277
 rc_AA134968_at AA134968 289 EST 12.11 up 0.00079
 rc_AA134985_at AA134985 290 EST 12.11 up 0.00318
 rc_AA135407_f_at AA135407 292 endogenous retroviral protease 3.64 up 0.01086
 rc_AA135871_at AA135871 294 EST 3.39 up 0.01544
 rc_AA135894_at AA135894 295 retinoic acid induced 3 14.27 up 0.00558
 rc_AA136547_at AA136547 302 EST 3.51 up 0.00308
 rc_AA143493_at AA143493 310 pleckstrin 2 (mouse) homolog 4.58 up 0.01037
 rc_AA143763_at AA143763 311 EST 18.09 up 0.00347
 rc_AA146619_at AA146619 312 EST 4.87 up 0.00863
 rc_AA147084_at AA147084 314 proliferation-associated 2G4, 38kD 4.4 up 0.0045
 rc_AA147439_s_at AA147439 315 EST 5.01 up 0.00336 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_AA148885_at AA148885 320 minichromosome maintenance deficient (S. cerevisiae) 4 6.39 up 0.0125
 rc_AA148977_at AA148977 322 ESTr 3.64 up 0.02911
 rc_AA149889_at AA149889 326 neighbor of A-kinase anchoring protein 95 3.34 up 0.02054
 rc_AA150053_at AA150053 327 EST 3.71 up 0.00102
 rc_AA151182_at AA151182 332 EST 3.51 up 0.00043
 rc_AA151428_s_at AA151428 335 matrix metalloproteinase 23B 7.15 up 0.00056
 rc_AA151778_at AA151778 338 claudin 7 5.77 up 0.00002
 ATP synthase, H⁺ transporting, mitochondrial F₀ complex, up
 rc_AA156187_at AA156187 339 ESTsubunit b, isoform 1 23.24 up 0.00006
 rc_AA156243_at AA156243 340 serine protease, umbilical endothelium 41.44 up 0.00139
 rc_AA156450_at AA156450 342 EST 3.33 up 0.00587
 rc_AA157818_f_at AA157818 349 endogenous retroviral protease 25.99 up 0.00153
 rc_AA158234_at AA158234 351 EST 17.04 up 0.00711
 rc_AA158795_at AA158795 352 EST 3.07 up 0.00057
 rc_AA159525_at AA159525 354 EST 49.39 up 0.00062
 rc_AA161043_at AA161043 356 tetraspan 1 18.8 up 0.00015
 rc_AA161292_s_at AA161292 357 interferon, alpha-inducible protein 27 13.84 up 0.00004
 rc_AA164252_f_at AA164252 358 VGF nerve growth factor inducible 3.41 up 0.00154
 NADH dehydrogenase (ubiquinone) Fe-S protein 6 (13kD) up
 rc_AA169837_at AA169837 364 (NADH-coenzyme Q reductase) 3.17 up 0.03038
 rc_AA171760_at AA171760 367 EST 17.86 up 0
 rc_AA171939_at AA171939 368 EST 4.67 up 0.00104
 rc_AA172076_at AA172076 369 EST 3.06 up 0.00326
 rc_AA173430_at AA173430 371 EST 4.32 up 0.04362
 rc_AA179298_at AA179298 378 stomatin-like protein 2 3.72 up 0.00299
 rc_AA179787_at AA179787 380 polyglutamine binding protein 1 6.44 up 0.00206
 rc_AA179845_at AA179845 381 EST 5.77 up 0.01414
 rc_AA181600_at AA181600 384 EST 5.38 up 0.03316
 rc_AA182001_i_at AA182001 386 EST 3.56 up 0.00945
 rc_AA187938_at AA187938 391 EST 3.86 up 0.00512 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.
 <P>Affy ID Genbank Seq Id known Gene Name Flod Chang Direction Pvalue
 rc_AA18838_i_at AA188378 392 EST 9.56 up 0.00271
 rc_AA188378_f_at AA188378 392 EST 5.54 up 0.01359
 rc_AA189015_at AA189015 394 EST 5.27 up 0.00004
 rc_AAS191708_at AA191708 400 EST 3.87 up 0.01904
 rc_AA192755_at AA192755 401 EST 3.13 up 0.00442
 rc_AA194237_at AA194237 408 EST 3.13 up 0.00212
 rc_AA194724_at AA194724 409 endonuclease G 3.09 up 0.04011
 rc_AA196790_at AA196790 421 EST 7.64 up 0.00287
 rc_AA204927_at AA204927 425 tropomyosin 1 (alpha) 7.09 up 0.0074
 rc_AA211483_at AA211483 435 EST 44.07 up 0.00175
 rc_AA2211851_f_at AA2211851 436 EST 3.66 up 0.00789
 rc_AA213696_at AA213696 437 poly(A)-binding protein, cytoplasmic 1 24.65 up 0.00001
 AA215299_s_at AA215299 439 U6 snRNA-associated Sm-like protein LSm7 15.84 up 0.00001
 rc_AA215468_s_at AA215468 441 ADP-ribosylation factor-related protein 1 3.9 up 0.04549
 rc_AA218663_at AA218663 444 acid-inducible phosphoprotein 3.26 up 0.0357
 AA224502_at AA224502 451 EST 4.12 up 0.0694
 rc_AA226932_at AA226932 453 DKFZP564F0923 protein 6.84 up 0.00405
 rc_AA227560_at AA227560 458 EST 12.81 up 0.01693
 rc_AA227926_at AA227926 460 EST 6.81 up 0.01701
 rc_AA233886_s_at AA233886 475 D site of albumin promoter (albumin D-box) binding protein 3.38 up 0.0218
 rc_AA233959_i_at AA233959 477 EST 19.69 up 0.00101
 rc_AA234096_at AA234096 479 EST 23.72 up 0.00018
 rc_AA23462_at

AA234362 481 EST 3.89 up 0.03524
 rc_AA235707_at AA235707 500 ST 9.17 up 0.00005
 rc_AA236037_at AA236037 506 EST 5.74 up 0.0091
 rc_AA236533_s_at AA236533 514 ecotropic viral integration site 1 4.1 up 0.02882
 rc_AA236714_f_at AA236714 516 nuclear mitotic apparatus protein 1 4.35 up 0.00083
 rc_AA237017_at AA237017 521 KIAA 1068 protein 3.52 up 0.00976
 rc_AA243133_at AA243133 525 serine/threonine kinase 15 7.73 up 0.04328
 rc_AA243173_at AA243173 526 EST 8.75 up 0.00003 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 AA249819_s_at AA249819 535 EST 5.09 up 0.00136
 rc_AA251230_at AA251230 540 EST 4.75 up 0.00054
 rc_AA251299_s_at AA251299 541 KIAA0014 gene product 16.86 up 0.00046
 rc_AA251909_at AA251909 549 EST 3.35 up 0.03937
 rc_AA252994_at AA252994 557 apoptosis inhibitor 4 (survivin) 3.55 up 0.00075
 rc_AA253011_f_at AA253011 558 KIAA0713 protein 4.73 up 0.01944
 AA253330_s_at AA253330 562 adaptor-related protein complex 1, gamma 1 subunit 3.87 up 0.00708
 rc_AA253473_at AA253473 567 EST 15.23 up 0.00171
 rc_AA256273_at AA256273 577 EST 4.13 up 0.03874
 rc_AA256642_at AA256642 582 EST 11.17 up 0.00035
 rc_AA258482_s_at AA258482 596 zinc finger protein 3.17 up 0.04606
 rc_AA261907_at AA261907 603 DKFZP566E144 protein 4.54 up 0.02289
 rc_AA262477_at AA262477 608 ribonuclease HI, large subunit 4.87 up 0.00005
 rc_AA262887_at AA262887 610 EST 5.4 up 0.04719
 rc_AA262943_at AA262943 611 EST 13.42 up 0.00234
 rc_AA262969_f_at AA262969 613 ferritin, heavy polypeptide 1 4.49 up 0.00013
 AA263044_s_at AA263044 615 H2A histone family, member Y 4.13 up 0.00024
 rc_AA278817_at AA278817 618 EST 4.22 up 0.00061
 rc_AA278838_s_at AA278838 620 EST 3 up 0.02832
 rc_AA279177_at AA279177 624 lymphocyte antigen 75 6.05 up 0.01821
 rc_AA279840_at AA279840 632 titin-cap (telethonin) 5.58 up 0.01253
 rc_AA280283_s_at AA280283 637 EST 4.99 up 0.02644
 rc_AA280734_i_at AA280734 639 KIAA0618 gene product 9.64 up 0.00003
 rc_AA280928_at AA280928 642 EST 3.27 up 0.04625
 rc_AA282149_s_at AA282149 654 huntingtin interacting protein-1-related 4.19 up 0.00091
 rc_AA282247_at AA282247 657 EST 8 up 0.00014
 rc_AA283085_s_at AA283085 667 EST 4.93 up 0.00382
 rc_AA284879_at AA284879 679 EST 24.68 up 0.0001
 rc_AA284945_at AA284945 680 EST 5.98 up 0.00026
 rc_AA287022_s_at AA287022 685 thymidine kinase 1, soluble 4.51 up 0.02582
 rc_AA287347_at AA287347 687 EST 5.47 up 0.00034 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_AA287393_at AA287393 688 EST 5.68 up 0.00062
 rc_AA290674_s_at AA290674 692 eukaryotic translation initiation factor 4E binding protein 1 11.59 up 0.00036
 rc_AA291137_at AA291137 694 EST 5.21 up 0.00685
 rc_AA291139_at AA291139 695 EST 8.69 up 0.04573
 rc_AA291168_at AA291168 696 EST 40.67 up 0.0065
 AA291456_s_at AA291456 700 EST 3.96 up 0.03633
 rc_AA291659_at AA291659 702 EST 3.83 up 0.1934
 rc_AA292379_at AA292379 708 EST 6.04 up 0.00568
 rc_AA292659_at AA292659 710 EST 3.48 up 0.00037
 rc_AA292765_at AA292765 712 ZW10 interactor 7.14 up 0.02623
 rc_AA292788_s_at AA292788 714 EST 7.69 up 0.00967
 rc_AA292931_at AA292931 715 EST 3.97 up 0.00067
 rc_AA293719_at AA293719 720 EST 4.69 up 0.2181
 AA295819_s_at AA295819 722 EST 8 up 0.01793
 AA29786_at AA29786 727 EST 4.65 up 0.02821
 AA306121_at AA306121 729 EST 4.85 up 0.00381
 AA307748_s_at AA307748 730 EST 3.7 up 0.00001
 AA320369_s_at AA320369 735 chromosome 19 open reading frame 3 4.33 up 0.00554
 AA328993_s_at AA328993 738 EST 3.66 up 0.00146
 rc_AA331393_at AA331393 739 EST 16.73 up 0.00848
 rc_AA335091_at AA335091 740 EST 5.28 up 0.0009
 rc_AA335191_f_at AA335191 741 creatine kinase, brain 47.35 up 0.00419
 rc_AA338729_at AA338729 743 EST 3.33 up 0.00046
 rc_AA338889_f_at AA338889 745 actin related protein 2/3 complex, subunit 4 (20 KD) 10.77 up 0.03782
 AA364267_at AA364267 762 EST 5.01 up 0.00255
 rc_AA370163_at AA370163 766 EST 3.34 up 0.00643
 rc_AA372018_at AA372018 768 EST 14.3 up 0.00178
 AA372630_s_at AA372630 769 differentially expressed in

hematopoietic lineages 25.49 up 0.01743
 AA384184_s_at AA384184 774 KFZP586B0519 protein 3.38 up 0.01209
 rc_AA394121_at AA394121 778 lamin receptor 1 (67kD, ribosomal protein SA) 23.78 u 0.00099 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_AA397906_at AA397906 782 DKFZP4341216 protein 3.2 up 0.00138
 rc_AA397916_f_at AA397916 784 EST 3.27 up 0.02895
 rc_AA398205_at AA398205 789 EST 4.17 up 0.00004
 rc_AA398761_s_at AA398761 799 EST 3.43 up 0.0726
 rc_AA398908_at AA398908 801 EST 38.69 up 0.01089
 rc_AA399226_at AA399226 803 tight junction protein 3 (zona occludens 3) 3.59up 0.02002
 rc_AA400271_at AA400271 814 EST 3.51 up 0.00742
 rc_AA401958_at AA401958 832 EST 3.62 up 0.01232
 rc_AA402495_at AA402495 838 EST 4.91 up 0.00235
 AA402937_at AA402937 843 EST 3.11 up 0.00182
 rc_AA402968_at AA402968 844 EST 3.1 up 0.00453
 rc_AA403159_at AA403159 845 Ste-20 related kinase 7.33 up 0.00187
 rc_AA404338_at AA404338 849 EST 01.9 up 0.00668
 rc_AA405310_at AA405310 856 EST 3.23 up 0.00138
 rc_AA405460_at AA405460 857 EST 4.02 up 0.03492
 rc_AA405715_at AA405715 862 hypothetical protien 4.68 up 0.00898
 rc_AA405791_at AA405791 864 EST 21.22 up 0
 rc_AA406145_f_at AA406145 870 EST 6.71 up 0.00047
 rc_AA406218_at AA406218 872 EST 4.88 up 0.02194
 rc_AA406385_at AA406385 876 DKFZP564B0769 protien 3.21 up 0.00724
 rc_AA406542_at AA406542 878 EST 8.27 up 0.00724
 rc_AA410469_at AA410469 883 EST 6.3 up 0.00103
 rc_AA410508_at AA410508 885 EST 16.04 up 0.02635
 rc_AA10962_s_at AA10962 887 peroxisome proliferative activated receptor, delta 3.45 up 0.04574
 rc_AA410972_at AA410972 888 EST 3.12 up 0.00023
 rc_AA411502_at AA411502 889 EST 16.42 up 0.00241
 rc_AA411685_at AA411685 890 EST 3.83 up 0.00417
 rc_AA411813_at AA411813 893 postmeiotic segregation increased 2-like 11 6.76 up 0.03499
 rc_AA412301_at AA412301 899 EST 4.57 up 0.00026
 rc_AA412403_at AA412403 900 EST 3.09 up 0.00047
 rc_AA412405_s_at AA412405 901 EST 13.82 up 0.01021 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_AA412720_at AA412720 905 EST 3.6 up 0.01396
 rc_AA416963_at AA416963 911 EST .69 up 0.03956
 rc_AA416973_at AA416973 913 EST 3.61 up 0.0091
 rc_AA419217_at AA419217 923 DKFZP586E1422 protein 6.77 up 0.00045
 rc_AA421562_at AA421562 934 anterior gradient 2 (Xenopus laevis) homolog 56.3 up 0.0041
 rc_AA42163_at AA42163 935 EST 3.05 up 0.00487
 rc_AA422049_at AA422049 937 EST 3.38 up 0.0067
 rc_AA422086_at AA422086 938 EST 10.71 up 0.03418
 rc_AA422150_at AA422150 939 cytochrome P540 family member predicted from ESTs 17.14 up 0.00108
 rc_AA424029_at AA424029 943 EST 8.68 up 0.00081
 rc_AA424487_at AA424487 945 EST 38.41 up 0.00002
 rc_AA424881_at AA424881 949 EST 6.3 up 0.00556
 rc_AA425279_at AA425279 951 quiescin Q66.15 up 0.00083
 rc_AA425401_at AA425401 954 serine/threonine kinase 24 (Ste20, yeast homolog) 3.22 up 0.00625
 rc_AA425852_s_at AA425852 958 EST 7.78 up 0.00239
 rc_AA425852_i_at AA425852 958 EST 4.8 up 0.03874
 rc_AA426447_at AA426447 965EST 4.23 up 0.0309
 rc_AA426521_at AA426521 967 Sjogren's syndrome nuclear autoantigen 1 3.47 up 0.01161
 rc_AA427442 at AA427442 971 guanine nucleotide regulatory facot 3.43 up 0.01547
 AA427468_s_at AA427468 973 claudin 4 84.43 up 0
 rc_AA427636_at AA427636 976 EST 19.23 up 0.00145
 rc_AA427825_at AA427825 981 EST 3.32 up 0.01615
 rc_aa427925_s_at AA427925 982 EST 3.23 up 0.01806
 rc_AA427946_at AA427946 983 dynein, axonemal, light polypeptide 4 3.01 up 0.00001
 AA428172_f_at AA428172 986 Notch (Drosophila) homolog 3 9.53 up 0.02562
 rc_AA428964_at AA428964 993 kallikrein 10 21.83 up 0.02324
 rc_AA429009_at AA429009 994 srine protease inhibitor, Kunitz type 1 30.04 up 0.00001
 rc_AA429470_at AA429470 996 EST 3.67 up 0.00782
 rc_AA429472_at AA429472 997 DKFZP434P106 protein 8.27 up 0.00208
 rc_AA429636_at AA429636 1001 hexokinase 2 10.43 up 0.00597
 AA429825_at AA429825 1003 DKFZP566B023 protein 6.63 up 0.00032 Table 6A Genes up regulated in metastatic tissue versus normal sample set

2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue

rc_AA429890_s_at AA429890 1004 cisplatin resistance associated 12.51 up 0.00053

rc_AA430032_at AA430032 1009 pituitary tumor-transforming 1 16.87 up 0.00659

rc_AA430048_at AA430048 1012 KIAA0160 protein 6.27 up 0.00631
 rc_AA430674_at
AA430674 1018 EST 15.11 up 0.00293
 rc_AA431719_at AA431719 1025 EST 4.25 up
0.00015
 rc_AA431776_at AA431776 1027 EST 3.24 up 0.01814
 rc_AA431873_at
AA431873 128 EST 4.03 up 0.00785
 rc_AA432162_at AA432162 1029 DKFZP586B2022
protein 3.48 up 0.03851
 rc_AA433930_at AA433930 1032 chondroitin 4-sulfotransferase 7.68 up
0.02445
 rc_AA434418_at AA434418 1036 KIAA1115 protein 5.12 up 0.00498

rc_AA435526_s_at AA435526 1037 transferrin receptor (p90, CD71) 3.69 up 0.00139

rc_AA435665_at AA435665 1040 EST 8.66 up 0.00001
 rc_AA436027_at AA436027 1050 EST
3.71 up 0.003676
 rc_AA436473_s_at AA436473 1052 EST 3.03 up 0.00133

c_AA436616_at AA436616 1056 EST 3.18 up 0.04402
 rc_AA437368_at AA437368 1063 EST
3.75 up 0.01317
 rc_AA437387_s_at AA437387 1064 EST 3.81 up 0.01478

rc_AA441911_at AA441911 1066 EST 3.81 up 0.01478
 AA44205_s_at AA442054 1067
phospholipase C, gamma 1 (formerly subtype 148) 16.89 up 0.00205
 rc_AA442763_at Aa442763
1072 cyclin B2 5.09 up 0.02168
 rc_AA43271_at AA43271 1073 KiAA0546 protein 3.6 up
0.01228
 rc_AA443316_s_at AA443316 1075 v-Ha-ras Harvey rat sarcoma viral oncogene
homolog 4.13 u 0.01729
 rc_AA443941_at AA443941 1085 tumor suppressing subtransferable
candidate 1 3.57 up 0.01685
 rc_AA446949_at AA446949 1096 EST 3.41 up 0.03411

rc_AA446968_at AA446968 1097 EST 3.45 up 0.02232
 rc_AA447118_s_at AA447118 1099
EST 3.03 up 0.01702
 rc_AA447683_at AA447687 1104 EST 11.42 up 0.00362

rc_AA447732_at AA447732 1105 EST 3.3 up 0.00591
 rc_AA447991_at AA447991 1112 EST
4.99 up 0.00173
 rc_aa449073_s_at AA449073 1117 EST 6.89 up 0.01445
 rc_AA449122_at
AA449122 1119 EST 3.65 up 0.00369 Table 6A. Genes up regulated in metastatic tissue versus normal
sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction
Pvalue
 rc_AA449456_at AA449456 1126 EST 6.29 up 0.00087
 rc_AA449456_at
AA449458 1127 EST 3.22 up 0.03098
 rc_AA449475_at AA449475 1128 EST 3.06 up
0.00291
 rc_AA449479_at AA449479 1129 EST 3.09 up 0.03495
 rc_AA450247_at
AA450247 1133 EST 5.27 up 0.02833
 rc_AA451676_at AA451676 1135 EST 14.72 up
0.00056
 hepatocellular carcinoma associated proein; breast cancer
 rc_AA451680_at
AA451680 1136 associated gene 1 3.55 up 0.00708
 rc_AA451877_at AA451877 1138 EST 8.63
up 0.00489
 rc_AA452259_at AA452259 1143 EST 3.49 up 0.00114
 rc_AA452536_at
AA452536 1145 v-ras similar leukemia viral oncogene homolog A (ras related) 5.6up 0.00481

AA452724_at AA452724 1149 programmed cell death 5 7.2 up 0.00908
 rc_AA453477_at
Aa453477 1153 X-prolyl aminopeptidase (aminopeptidase P)-like 4.23 up 0.0001

rc_AA453783_s_at AA453783 1158 EST 6.16 up 0.00167
 rc_AA454597_s_at AA454597 1166
EST 3.63 up 0.0067
 rc_AA454710_at AA454710 1168 EST 3.42 up 0.00653

AA454908_s_at AA454908 1171 KiAA0144 gene product 9.3 up 0.00539
 rc_AA455521_s_at
AA455521 1178 E2F transcription factor 5, p130-binding 4.6 up 0.00773
 rc_AA455522_s_at
AA455522 1179 EST 3.83 up 0.00017
 rc_aa458852_f_at AA458852 1203 KiAA0440 protein 3.2
up 0.00038
 rc_AA458890_at AA458890 1206 EST 3.36 up 0.00303
 rc_AA459254_at
AA459254 1211 EST 5.36 up 0.0259
 rc_AA459310_r_at AA459310 1214 EST 3.45 up
0.00179
 rc_AA459388_s_at AA459388 1215 copine I 5.23 up 0.00691
 rc_AA459703_at
AA459703 1222 v-myc avian myelocytomatosis viral oncogene homolog 4.75 up 0.02413

rc_AA459961_at AA459961 1223 EST 3.24 up 0.00316
 rc_AA460017_i_at AA460017 1225
EST 10.76 up 0.00106
 rc_AA460017_f_at AA460017 1225 EST 3.61 up 0.00109

rc_AA461187_at AA461187 1236 EST 8.15 up 0.00068 Table 6A. Genes up regulated in metastatic
tissue versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change
Direction Pvalue
 rc_AA461473_at AA461473 1242 nebulin 3.35 up 0.03855

rc_AA461476_at AA461476 1243 ET 4.12 up 0.00871
 rc_AA463234_at AA463234 1246

KIAA0792 gene product 5.94 up 0.01182
 mannosyl (alpha-1,6-)-glycoprotein beta-1,2-N
 rc_AA463725_at AA463725 1249 acetylglucosaminyltransferase 7.4 up 0.04715
 rc_AA463861_at AA463861 1251 EST 24.79 up 0.00096
 rc_AA4614414_i at AA464414 1258 EST 4.99 up 0.00529
 rc_AA464698_at AA464698 1262 EST 3.24 up 0.04854
 rc_AA464963_at AA464963 1265 EST 5.01 up 0.00107
 BUB3 (budding uninhibited by benzimidazoles 3, yeast)
 AA471278_at AA471278 1277 homolog 5.14 up 0.00873
 rc_AA476216_at AA476216 1279 EST 4.97 up 0.00359
 rc_AA478017_at AA478017 1295 zyxin 6.15 up 0.01625
 rc_AA478300_at AA478300 1298 CD39-like 2 6.15 up 0.01625
 rc_AA478415_at AA478415 1299 EST 4.56 up 0.00095
 rc_AA478599_at AA478599 1304 G proteon-coupled receptor 56 3.31 up 0.00182
 rc_AA479044_s at Aa479044 1307 EST 6.9 up 0.04668
 rc_AA479727_s at AA479727 1315 EST 6.06 up 0.00389
 rc_AA479797_at AA479797 1316 EST 7.93 up 0.00006
 rc_AA479945_s at AA479945 1319 plakophilin 3 3.17 up 0.01767
 rc_AA482007_at AA48207 1331 EST 3.49 up 0.00167
 protein kinase related to S. cerevisiae STE20, effector for
 rc_AA482127_at AA482127 1333 Cdc42Hs 4.88 up 0.00017
 rc_AA482224_f at AA482224 1334 putative type II membrane protein 4.62 up 0.0105
 AA482319_f at AA482319 1335 putative tye II membrane protein 5.11 up 0.00177
 rc_AA482546_s at AA482546 1336 KIAA0124 protein 4.41 up 0.00604
 rc_AA482613_at AA482613 1338 DKFZP434B203 protein 4.14 up 0.00186
 rc_AA485405_at AA485405 1343 EST 5.35 up 0.03475
 rc_AA485697_at AA485697 1346 EST 14.74 up 0.00102
 rc_AA488987_s at AA488987 1365 synaptogyrin 2 3.24 up 0.01444
 rc_AA489707_at AA489707 1371 EST 3.47 up 0.3433 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.
 <P>Affy ID Genbank Seq Id Known Gene Name Fold Change Direction Pvalue
 rc_AA489712_at AA489712 1372EST 4.93 up 0.00726
 rc_AA490212_at AA490212 1375 H2A histone family, member Y 3.71 up 0.01226
 rc_AA490494_at AA490494 1377 EST 5.16 up 0.01696
 rc_AA491223_at AA491223 1389 EST 3.03 up 0.00557
 rc_AA496204_at AA496204 1397 EST 3.69 up 0.01097
 rc_AA496245_at AA496245 1398 EST 3.96 up 0.0039
 v-erb-b2 avian erythroblastic leukemia viral oncogene homolog
 rc_AA496981_at AA496981 1404 3 4.93 up 0.01096
 rc_AA497031_at AA497031 1407 EST 11.05 up 0.04381
 rc_AA504111_at AA504111 1409 EST 3.81 up 0.00684
 rc_AA504270_at AA504270 1411 EST 4.96 up 0.01919
 AA504413_at AA%04413 1413 EST 3.35 up 0.00079
 rc_AA504806_at AA504806 1416 EST 3.54 up 0.00221
 rc_AA598405_at AA598405 1424 membrane interacting protein of RGS16 4.69 up 0.0122
 rc_AA498506_s at AA598506 1430 KIAA0179 protein 3.17 up 0.01694
 rc_AA598712 at AA598712 1436 EST 3.03 up 0.03656
 rc_AA598988_at AA598988 1442 EST 4.32 up 0.00044
 rc_AA599244_at AA599244 1448 KIAA0530 protein 3.39 up 0.01246
 rc_AA599522_f at AA599522 1452 squamous ell carcinoma antigen recognised by T cells 6.75 up 0.04229
 rc_AA608579_s at AA608579 1464 paired-like hmeodomain transcritpion factor 2 4.29 up 0.04435
 rc_AA608897_at AA608897 1473 EST 9.92 up 0.0087
 rc_AA608965_at AA608965 1474 Hemansky-Pudlak syndrome 3.19 up 0.00204
 rc_AA609008_at AA609008 1475 EST 3.46 up 0.02935
 rc_AA609013_s at AA609013 1477 dipeptidase 1 (renal) 10.17 up 0.00109
 rc_AA606914_at AA60964 1487 EST 6.5 up 0.00406
 rc_AA609786_s at AA6076 1491 nucleolar protein 1 (120kD) 4.75 up 0.00261
 rc_AA610053_at AA610053 1496 EST 7.01 up 0.00003
 rc_AA61116_i at AA610116 1499 tetraspan NEt-6 protein 33.68 up 0.00171
 rc_AA620466_at AA620466 1502 EST 5.14 up 0.00004 Table 6A. Genes up regulated in metastatic tissue versus normal sample set s.
 <P>Affy ID Genbank Seq ID Known Gene Name Fld Change Direction Pvalue
 rc_AA620881_at AA620881 1510 trinucleotide repeat containing 3 8.66 up 0.00735
 rc_AA620995_at AA620995 1512 EST 3.74 up 0.03414
 rc_AA621277_at AA621277 1520 EST 3.81 up 0.00194
 rc_AA621780_at AA621780 1530 CGI-96 protein 3.65 up 0.01582
 AB0005484_at AB000584 1533 prostate differentiation fator 4.7 up 0.00071
 AB002533_at AB002533 1539 karyopherin alpha 4 (importin alpha 3) 6.38 up 0.00003
 AB006781_s at AB006781 1540 lectin, galactoside-binding, soluble, 4 (galectin 4) 7.05 up 0.00913
 AF001294_at

AF001294 1544 tmor suppressing subtransferable candidate 3 7.45 up 0.00009
 AF003521_at
 AF003521 15645 jagged 2 11.26 up 0.00008
 AF004709_at AF004709 1547 mitogen-activated
 protein kinase 13 3.92 up 0.0009
 stress-associated endoplasmic reticulum protein 1;
 ribosome
 C00021_s_at C00021 1551 associated membrane protein 4 3.33 up 0.00215

 C01766_s_at C01766 1559 EST 13.67 up 0.00003
 rc_C13992_f_at C13992 1564 EST 6.39 up
 0.00059
 rc_C14051_f_at C14051 1565 phosphoprotein enriched in astrocytes 15 3.68 up
 0.01453
 rc_C14098_f_at C14098 1566 EST 3.53 up 0.04401
 rc_C14348_at C14348 1568
 EST 4.06 up 0.00111
 C14412_s_at C14412 1569 HSPC038 protein 3.9 up 0.00036

 rc_C14756_f_at C14756 1570 MLN51 protein 5.36 up 0.00001
 rc_C15324_f_at C15324 1574
 EST 5.22 up 0.00344
 rc_C21248_at C21248 1585 pituitary tumor-transforming 1 3.85 up
 0.00456
 D00017_at D00017 1587 annexin A2 11.38 up 0
 interleukin 2 receptor, gamma
 (severe combined 0
 D11086_at D11086 1595 immunodeficiency)
 heterogeneous nuclear
 ribonucleoprotein U (scaffold
 D13413_ma1_s_at D13413 1604 attachment factor A) 4.79 up
 0.00092
 D13639_at D13639 1607 cyclin D2 7.49 up 0.01641
 D14520_at D14520 1613
 basic transcription element binding protein 2 4.93 up 0.00004
 D14530_at D14530 1614 ribosomal
 protein S23 3.1 up 0.00331
 D14657_at D14657 1615 KIAA0101 gene product 3.7 up
 0.04079
 rc_D19737_at D19737 1623 golgi autoantigen, golgin subfamily a, 3 3.44 up 0.02212
 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.
 <P>Affy ID
 Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_D20464_at D20464 1625
 bromodomain adjacent to zinc finger domain, 2B 3.27 up 0.04897
 rc_D20906_at D20906 1627
 EST 5.18 up 0.02189
 minichromosome maintenance deficient (S. cerevisiae) 2
 D21063_at
 D21063 1628 (mitotin) 3.83 up 0.00983
 D21261_at D21261 1629 transgelin 2 3.46 up
 0.00685
 D23660_at D23660 1630 ribosomal protein L4 3.22 up 0.00316
 D25216_at
 D25216 1631 KIAA0014 gene product 3.17 up 0.02125
 D25274_at D25274 1632 EST 3.39 up
 0.00238
 D25328_at D25328 1633 phosphofructokinase, platelet 3.17 up 0.04925

 rc_D25560_i_at D25560 1634 EST 4.72 up 0.00661
 D26129_at D26129 1635 ribonuclease,
 RNase A family, 1 (pancreatic) 5.68 up 0.03827
 neuroblastoma candidate region, suppression of
 tumorigenicity
 D28124_at D28124 1636 1 6.38 up 0.00015
 D31094_at D31094 1639 G8
 protein 4.41 up 0.04845
 D31417_at D31417 1645 secreted protein or unknown function 4.56 up
 0.00014
 D38073_at D38073 1651 minichromosome maintenance deficient (S. cerevisiae) 3 3.65
 up 0.01869
 D38548_at D38548 1655 KIAA0076 gene product 4.5 up 0.00036
 D38583_at
 D38583 1656 S100 calcium-binding protein A11 (calgizzarin) 18.7 up 0.00003
 D42085_at
 D42085 1658 KIAA0095 gene product 3.83 up 0.00036
 D43949_at D43949 1659 KIAA0082
 protein 3.32 up 0.0014
 D43950_at D43950 1660 chaperonin containing TCP1, subunit 5 (epsilon)
 3.61 up 0.00672
 D49400_at D49400 1667 ATPase, vacuolar, 14 kD 4.01 up 0.00287

 D50663_at D50663 1671 t-complex-associated-testis-expressed 1-like 1 4.09 up 0.00208

 D50913_at D50913 1672 KIAA0123 protein 3.32 up 0.01202
 D50914_at D50914 1673
 KIAA0124 protein 4.74 up 0.00752
 rc_D51112_s_at D51112 1675 collapsin response mediator
 protein 1 10.48 up 0.00076
 rc_D51133_f_at D51133 1676 tubulin, beta, 4 4.84 up 0.02875

 rc_D51276_f_at D51276 1678 leukemia-associated phosphoprotein p18 (stathmin) 4.81 up
 0.00514
 rc_D51287_f_at D51287 1680 ribosomal protein S12 3.3 up 0.02829

 rc_D51393_f_at D51393 1681 ribosomal protein L4 5.64 up 0.00074 Table 6A. Genes up regulated in
 metastatic tissue versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name
 Fold Change Direction Pvalue
 rc_D52632_f_at D52632 1683 ribosomal protein S6 3.12 up
 0.00498
 rc_D53139_f_at D53139 1684 ribosomal protein S28 4.38 up 0.0009

 rc_D54296_f_at D54296 1685 KIAA0255 gene product 3.8 up 0.01059
 D55716_at D55716 1686
 minichromosome maintenance deficient (S. cerevisiae) 7 6.6 up 0.00151
 rc_D57489_at D57489
 1689 chaperonin containing TCP1, subunit 7 (eta) 4.08 up 0.00001
 rc_D59322_f_at D59322 1694
 EST 4.18 up 0.00006
 rc_D59847_at D59847 1701 EST 3.09 up 0.02206
 rc_D60811_s_at
 D60811 1704 eST 3.22 up 0.0098
 platelet-activating factor acetylhydrolase, isoform Ib,
 gamma
 D63391_at D63391 1710 subunit (29kD) 3.91 up 0.00062
 D63486_at D63486 1712

KIAA0152 gene product 6.33 up 0.00078
 D63487_at D63487 1713 KIAA0153 protein 5.4 up 0.00027
 D63874_at D63874 1714 high-mobility group (nonhistone chromosomal) protein 1 3.64 up 0.00228
 D63880_at d63880 1715 KIAA0159 gene product 4.26 up 0.00253
 D78361_at D78361 1718 EST 3.14 up 0.00023
 D78676_at D78676 1719 EST 3.2 up 0.00635
 D79205_at D79205 1721 ribosomal protein L39 3.07 up 0.00021
 rc_D80237_s_at D80237 1729 actin related protein 2/3 complex, subunit 4 (20 kD) 3.27 up 0.00137
 rc_D80662_s_at D80662 1733 adaptor-related protein complex 1, gamma 2 subunit 3.43 up 0.100108
 rc_D80710_f_at D80710 1734 integral type I protein 7.08 up 0.00213
 rc_D80917_f_at D80917 1736 KIAA0670 protein/acinus 3.58 up 0.00007
 rc_D80946_f_at D80946 1737 SFRS protein kinase 1 8.53 up 0.00455
 5-aminoimidazole-4-carboxamide ribonucleotide
 D82348_at D82348 1744 formyltransferase/IMP cyclohydrolase 3.93 up 0.00037
 D82558_at D82558 1746 novel centrosomal protein RanBPM 5.94 up 0.00752
 D83735_at D83735 1747 calponin 2 10.42 up 0.00001
 trinucleotide repeat containing 11 (THR-associated protein, 230
 D83783_at D83783 1748 kDa subunit) 6.55 up 0.00176 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.
 <P>Affy ID Genbak Seq ID Known Gene Name Fold Change Direction Pvalue
 trinucleotide repeat containing 11 (THR-associated protein, 230
 D83783_at D83783 1748 kDa subunit) 3.33 up 0.00748
 D86956_at D86956 1753 heat shock 105kD 4 up 0.03013
 D86974_at D86974 1756 KIAA0220 protein 3.85 up 0.0161
 D87735_at D87735 1764 ribosomal protein L14 3.92 up 0.00015
 D87953_at D87953 1765 N-myc downstream regulated 6.12 up 0.00033
 D88154_at D88154 1766 villin-like 4.18 up 0.00051
 rc_F01444_f_at F01444 1770 KIAA0440 protein 6.78 up 0.00028
 rc_F01568_at F01568 1772 EST 3.24 up 0.0018
 rc_F02800_at F02800 1780 EST 3.45 up 0.03238
 rc_F02863_at F02863 1782 EST 3.21 up 0.01039
 rc_F04320_s_at F04320 1786 replication factor C (activator 1) 4 (37kD) 3.63 up 0.01119
 rc_F04444_at F04444 1788 EST 4.57 up 0.01132
 rc_F04531_s_at F04531 1791 Kell blood group precursor (McLeod phenotype) 7.79 up 0.03205
 rc_F04674_at F04674 1793 KIAA0746 protein 8.2 up 0.00028
 rc_F09297_s_at F09297 1800 EST 3.94 up 0.0016
 rc_F09394_s_at F09394 1803 KIAA0715 protein 22.89 up 0.01753
 rc_F09684at F09684 1805 EST 3.78 up 0.00277
 procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-
 rc_F09788_at F09788 1808 hydroxylase), alpha polypeptide II 4.14 up 0.00003
 rc_F13809_f_at F13809 1828 tropomyosin 1 (alpha) 7.62 up 0.00012
 rc_H04753_f_at H04753 1839 EST 3.38 up 0.02447
 rc_H04799_at H04799 1841 EST 3.71 up 0.04109
 rc_H05394_f_at H05394 1845 KIAA0266 gene product 4.06 up 0.0015
 rc_H05525_s_at H05525 1846 hypothetical protein 4.6 up 0.0033
 rc_H05625_f_at H05625 1847 EST 5.17 up 0.04551
 rc_H08863_at H08863 1859 hypothetical protein 3.48 up 0.00205
 rc_H09241_s_at H09241 1861 EST 4.17 up 0.00727
 rc_H09271_f_at H09271 1862 EST 5.06 up 0.0016
 rc_H09281_at H09281 1863 EST 6 up 0.00966
 rc_H13532_f_at H13532 1881 ribosomal protein L18a 3.97 up 0.00061 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_H17476_at H17476 1889 EST 3.44 up 0.00479
 rc_H18412_s_at H18412 1890 isocitrate dehydrogenase 3 (NAD+) gamma 4.37 up 0.00262
 rc_H18442_f_at H18442 1891 creatine kinase, brain 17.42 up 0.02391
 rc_H20989_s_at H20989 1899 pyruvate kinase, muscle 11.37 up 0.0375
 rc_H24077_at H24077 1900 EST 3.05 up 0.0324
 rc_H27188_f_at H27188 1908 collagen-binding protein 2 (colligen 2) 4.16 up 0.02073
 rc_H28333_f_at H28333 1912 melanoma adhesion molecule 3.11 up 0.00172
 rc_H29565_at H29565 1913 EST 3.89 up 0.01856
 rc_H38240_s_at H38240 1916 thrombospondin 2 4.28 up 0.0066
 rc_H38568_s_at H38568 1918 EST 4.86 up 0.0003
 rc_H42321_f_at H42321 1928 ribosomal protein L18a 3.23 up 0.01102
 H43286_s_at H43286 1929 gamma-aminobutyric acid (GABA) B receptor, 1 5.02 up 0.01972
 rc_H43646_at H43646 1930 H2A histone family, member Y 4.6 up 0.00147
 H46486_s_at H46486 1932 nesca protein 4.77 up 0.00421
 rc_H49637_s_at H49637 1940 EST 3.79 up 0.01092
 rc_H52673_s_at H52673 1943 BLC2-antagonist/killer 1 3.03 up 0.0393
 H53657_s_at H53657 1945 adenylate cyclase 3 3.98 up 0.0045
 H55437_at H55437 1948 kraken-

like 3.53 up 0.02344
 rc_H56345_r_at H56345 1950 EST 4.15 up 0.00488
 solute carrier family 2 (facilitated glucose transporter), member
 rc_H58873_s_at H58873 1961 1 57.98 up 0.00063
 rc_H59617_at H59617 1964 EST 3.3 up 0.04588
 rc_H75933_f_at H75933 1998 laminin receptor 1 (67kD, ribosomal protein SA) 5.81 up 0.00024
 rc_H78211_at H78211 2001 EST 6.73 up 0.02488
 rc_H78323_at H78323 2002 transcription factor Dp-1 3.69 up 0.00326
 high-mobility group (nonhistone chromosomal) protein isoforms
 rc_H81413_f_at H81413 2007 I and Y 5.82 up 0.00769
 rc_H88674_s_at H88674 2021 collagen, type 1, alpha 2 5.06 up 0.00866
 H89551_s_at H89551 2024 EST 9.94 up 0.00137
 rc_H93021_at H93021 2033 peptidylprolyl isomerase A (cyclophilin A) 3.31 up 0.0183
 rc_H93492_at H93492 2037 EST 3.94 up 0.01136 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_H93652_f_at H93652 2039 ribosomal protein S5 3.31 up 0.00788
 rc_H94471_at H94471 2042 occludin 43.09 up 0
 rc_H95233_s_at H95233 2048 serine protease inhibitor, Kunitz type, 2 47.06 up 0
 rc_H96975_at H96975 2057 EST 3.22 up 0.0141
 rc_H97013_at H97013 2059 ephrin-A4 9.14 up 0.00346
 rc_H97809_at H97809 2063 EST 4.05 up 0.00111
 rc_H98924_at H93924 2072 chromatin assembly factor 1, subunit A (p150) 3.53 up 0.02106
 rc_H99473_s_at H99473 2077 regulator of nonsense transcripts 1 5.37 up 0.00177 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 J03459_at J03459 2093 leukotriene A4 hydrolase 3.03 up 0.04041
 J03464_s_at J03464 2094 collagen, type 1, alpha 2 9.81 up 0.00028
 solute carrier family 25 (mitochondrial carrier; adenine
 J03592_at J03592 2096 nucleotide translocator), member 6 10.05 up 0
 J03827_at J03827 2100 nuclease sensitive element binding protein 1 4.45 up 0.00015
 membrane component, chromosome 1, surface marker 1
 J04152_ma1_s_at J04152 2107 (40kD glycoprotein, identified by monoclonal antibody GA733) 5.26 up 0.02466
 J04164_at J04164 2108 interferon induced transmembrane protein 1 (9-27) 12.37 up 0.00001
 AFFX-BioDn-3_at J04423 2109 EST 54.11 up 0.02774
 AFFX-BioDn-3_at J04423 2109 EST 48.05 up 0.02203
 AFFX-BioDn-3_at J04423 2109 EST 21.46 up 0.04283
 AFFX-BioB-3_at J04423 2109 EST 5.13 up 0.02791
 AFFX-BioB-5_at J04423 2109 EST 4.47 up 0.02754
 AFFX-BioDn-3_st J04423 2109 EST 4.35 up 0.01245
 J04469_at J04469 2111 creatine kinase, mitochondrial 1 (ubiquitous) 7.9 up 0.00705
 J04823_ma1_at J04823 2115 cytochrome c oxidase subunit VIII 3.35 up 0.00075
 J05257_at J05257 2118 dipeptidase 1 (renal) 12.02 up 0.02099
 J05582_s_at J05582 2121 mucin 1, transmembrane 5.39 up 0.00056
 solute carrier family 2 (facilitated glucose transporter), member
 K03195_at K03195 2128 1 10.73 up 0.00139
 K03460_at K03460 2129 tubulin, alpha 1 (testis specific) 7.5 up 0.00002
 L03411_s_at L03411 2134 RD RNA-binding protein 3.97 up 0.00422
 L04483_s_at L04483 2136 ribosomal protein S21 4.2 up 0.00057
 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9
 L04490_at L04490 2137 (39kD) 5.22 up 0.02192 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.
 <P>Affy ID genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 L06499_at L06499 2141 ribosomal protein L37a 4.34 up 0.01103
 L06505_at L06505 2142 ribosomal protein L12 5 up 0.00163
 L08044_s_at L08044 2149 trefoil factor 3 (intestinal) 21.42 up 0.01674
 L08044_s_at L08044 2149 trefoil factor 3 (intestinal) 14.18 up 0.02124
 L09604_at L09604 2151 proteolipid protein 2 (colonic epithelium-enriched) 8.68 up 0
 L11566_at L11566 2156 ribosomal protein L18 4.29 up 0.00014
 L11669_at L11669 2157 tetracycline transporter-like protein 6.75 up 0.00101
 L12350_at L12350 2160 thrombospondin 2 3.78 up 0.00061
 L12711_s_at L12711 2161 transketolase (Wernicke-Korsakoff syndrome) 3.08 up 0.03362
 high-mobility group (nonhistone chromosomal) protein isoforms
 L17131_ma1_at L17131 2168 I and Y 20.57 up 0.00058
 L19527_at L19527 2169 ribosomal protein L27 3.54 up 0.00025
 L19605_at L19605 2170 annexin A11 6.38 up 0.00017
 macrophage migration inhibitory factor (glycosylation-inhibiting
 L19686_ma1_at L19686 2171 factor) 5.26 up 0.00562
 L20591_at L20591 2173 annexin A3 4.64 up 0.00065
 L20941_at L20941 2174 ferritin, heavy polypeptide 1 3.3 up 0.01172
 L21954_at L21954 2177 benzodiazapine receptor

(peripheral) 8.53 up 0.00001
 L23808_at L23808 2179 matrix metalloproteinase 12 (macrophage elastase) 6.18 up 0.02195
 L25081_at L25081 2180 ras homolog gene family, member C 3.67 up 0.00005
 L33075_at L33075 2195 IQ motif containing GTPase activating protein 1 3.83 up 0.00015
 L33842_rna1_at L33842 2197 IMP (inosine monophosphate) dehydrogenase 2 11.03 up 0.00001
 L33930_s_at L33930 2198 CD24 antigen (small cell lung carcinoma cluster 4 antigen) 9.16 up 0.01252
 transcription elongation factor B (SIII), polypeptide 1 (15kD,
 L34587_at L34587 2200 elongin C) 4.32 up 0.00287
 L36720_at L36720 2205 bystin-like 3.46 up 0.00094
 L38696_at L38696 2208 RNA-binding protein (autoantigenic) 3.7 up 0.00093
 thyroid receptor interacting protein 10 (CDC42-interacting
 L40379_at L40379 2210 protein) 3.87 up 0.00207
 L40904_at L40904 2212 peroxisome proliferative activated receptor, gamma 3.43 up 0.03511 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 L41351_at L41351 2214 protease, serine, 8 (prostasin) 6.34 up 0.01132
 L44538_at L44538 2217 EST 4.34 up 0.04319
 L76191_at L76191 2222 interleukin-1 receptor-associated kinase 1 5.66 up 0.00089
 L76200_at L76200 2223 guanylate kinase 1 3.24 up 0.0097
 AFFX-HUMRGE/M10098M10098 2231 EST 11.55 UP 0.00099
 AFFX-HUMRGE/M10098M10098 2231 EST 10.2 UP 0.00027
 AFFX-HUMRGE/M10098M10098 2231 EST 5.62 UP 0.00251
 AFFX-HUMRGE/M10098M10098 2231 EST 5.61 UP 0.01238
 AFFX-HUMRGE/M10098M10098 2231 EST 5.35 UP 0.00186
 AFFX-HUMRGE/M10098M10098 2231 EST 4.79 UP 0.00328
 AFFX-HUMRGE/M10098M10098 2231 EST 4.66 UP 0.00405
 AFFX-HUMRGE/M10098M10098 2231 EST 3.73 UP 0.01794
 M12125_at M12125 2241 tropomyosin 2 (beta) 10.83 up 0.00191
 M13934_cds2_at M13934 2255 ribosomal protein S14 3.99 up 0
 M14199_s_at M14199 2258 laminin receptor 1 (67kD, ribosomal protein SA) 7.01 up 0
 M14483_rna1_s_at M14483 2261 prothymosin, alpha (gene sequence 28) 4.46 up 0.00686
 M14949_at M14949 2264 related RAS viral (r-ras) oncogene homolog 3.11 up 0.00013
 M15205_at M15205 2265 thymidine kinase 1, soluble 3.75 up 0.00159
 M16364_s_at M16364 2269 creatine kinase, brain 12.69 up 0.03633
 M17733_at M17733 2280 thymosin, beta 4, X chromosome r.15 up 0.00009
 M17885_at M17885 2281 ribosomal protein, large, P0 3.92 up 0.00003
 M17886_at M17886 2282 ribosomal protein, large, P1 4.34 up 0.00004
 M18000_at M18000 2283 ribosomal protein S17 3.79 up 0.00004
 carcinoembryonic antigen-related cell adhesion molecule 6 (non
 M18728_at M18728 2285 specific cross reacting antigen) 44.82 up 0.00291
 M20471_at M20471 2289 clathrin, light polypeptide (Lca) 5.32 up 0.00344
 M22960_at M22960 2296 protective protein for beta-galactosidase (galactosialidosis) 4.49 up 0.00898
 M23613_at M23613 2301 nucleophosmin (nucleolar phosphoprotein B23, numatrin) 3.67 up 0.00977 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 guanine nucleotide binding protein (G protein), beta polypeptide
 M24194_at M24194 2302 2-like 1 4.55 up 0.00017
 M24485_s_at M24485 2304 glutathione S-transferase pi 10.2 up 0.00003
 M26708_s_at M26708 2311 prothymosin, alpha (gene sequence 28) 3.35 up 0.00064
 M27826_at M27826 2313 endogenous retroviral protease 26.36 up 0.00342
 AFFX-M27830_5_at M27830 2314 EST 15.53 up 0.00022
 AFFX-M27830_5_at M27830 2314 EST 14.86 UP 0.00043
 AFFX-M27830_5_at M27830 2314 EST 10.64 UP 0.00213
 AFFX-M27830_M_at M27830 2314 EST 9.8 UP 0.00041
 AFFX-M27830_M_at M27830 2314 EST 8.78 UP 0.00003
 AFFX-M27830_5_at M27830 2314 EST 8.2 UP 0.00294
 AFFX-M27830_M_at M27830 2314 EST 6.25 UP 0.00046
 AFFX-M27830_M_at M27830 2314 EST 5.78 UP 0.0017
 M29277_at M29277 2316 melanoma adhesion molecule 3.91 up 0.00112
 M29540_at M29540 2317 carcinoembryonic antigen-related cell adhesion molecule 5 36.57 up 0.0116
 M30496_at M30496 2324 ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase) 3.8 up 0.00478
 M31303_rna1_at M31303 2327 leukemia-associated phosphoprotein p18 (stathmin) 7.48 up 0.00021
 M31520_rna1_s_at M31520 2328 ribosomal protein S24 3.37 up 0.00077
 M31520_at M31520 2328 ribosomal protein S24 3.13 up 0.00014
 M32405_at

M32405 2334 ribosomal protein S15 4.01 up 0.00055
 M32886_at M32886 2335 sorcin 8.35 up 0.00215
 AFFX-HUMGAPDH/M33 M33197 2337 glyceraldehyde-3-phosphate dehydrogenase 3.31 up 0.00009
 M34182_at M34182 2340 protein kinase, cAMP-dependent, catalytic, gamma 4.51 up 0.00043
 M35252_at M35252 2343 transmembrane 4 superfamily member 3 39.12 up 0
 M36072_at M36072 2347 ribosomal protein L7a 3.1 up 0.00006
 S100 calcium-binding protein A10 (annexin II ligand, calpactin I,
 M38591_at M38591 2350 light polypeptide (p11) 14.87 up 0
 M38690_at M38690 2351 CD9 antigen (p24) 9.08 up 0.00059
 M55998_s_at M55998 2356 collagen, type I, alpha 1 6.99 up 0.00103 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 M57710_at M57710 2357 lectin, galactoside-binding, soluble, 3 (galectin 3) 27.12 up 0.00001
 M60784_s_at M60784 2366 small nuclear ribonucleoprotein polypeptide A 5.74 up 0.00126
 M60854_at M60854 2367 ribosomal protein S16 3.4 up 0.00001
 M62895_s_at M62895 2375 annexin A2, annexin A2 pseudogene 2 6.11 up 0.00013
 M64716_at M64716 2382 ribosomal protein S25 3.16 up 0.00039
 M68864_at M68864 2389 ORF 3.1 up 0.00603
 M77232_ma1_at M77232 2399 ribosomal protein S6 3.82 up 0.00045
 M77349_at M77349 2400 transforming growth factor, beta-induced, 68kD 4.81 up 0.00546
 M77836_at M77836 2401 pyrroline-5-carboxylate reductase 1 3.43 up 0.00759
 M79463_s_at M79463 2402 promyelocytic leukemia 4.88 up 0.01821
 M81757_at M81757 2406 ribosomal protein S19 5.46 up 0
 tyrosine 3-monooxygenase/tryptophan 5-monooxygenase
 M86400_at M86400 2410 activation protein, zeta polypeptide 5.62 up 0.00016
 M86667_at M86667 2411 nucleosome assembly protein 1-like 1 3.03 up 0.04853
 stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing
 M86752_at M86752 2412 protein) 7.32 up 0.00001
 M87339_at M87339 2415 replication factor c (activator 1) 4 (37kD) 4.07 up 0.00316
 M91083_at M91083 2419 chromosome 11 open reading frame 13 3.3 up 0.00163
 membrane component, chromosomal 4, surface marker (35kD
 M93036_at M93036 2422 glycoprotein) 16.45 up 0.00308
 M94250_at M94250 2426 midkine (neurite growth-promoting factor 2) 10.39 up 0.01818
 M94345_at M94345 2427 capping protein (actin filament), gelsolin-like 22.38 up 0.00003
 M96739_at M96739 2434 nescient helix loop helix 1 3.72 up 0.00015
 rc_N20198_s_at N20198 2440 ubiquitin-conjugating enzyme E2 variant 1 5.17 up 0.00508
 rc_N21359_at N21359 2442 ESWT 4.43 up 0.00078
 rc_N22015_at N22015 2448 EST 46.61 up 0.00025
 rc_N22107_at N22107 2449 EST 6.88 up 0.04259
 rc_N24899_at N24899 2461 EST 3.06 up 0.00353
 rc_N26186_at N26186 2468 EST 6.15 up 0.00135
 rc_N27186_at N27186 2470 EST 3.79 up 0.00112
 rc_N27334_at N27334 2471 EST 3.65 up 0.03437 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_N29888_at N29888 2483 EST 3.7 up 0.00226
 rc_N30436_f_at N30436 2484 EST 3.45 up 0.02356
 rc_N31570_at N31570 2486 TNF receptor-associated factor 5 10.39 up 0.00018
 rc_N31597_s_at N31597 2487 DKFZP564G2022 protein 4.44 up 0.00085
 N36432_at N36432 2507 erythrocyte membrane protein band 4.1-like 2 3.03 up 0.03086
 rc_N39099_at N39099 2508 EST 4.42 up 0.00643
 rc_N39237_at N39237 2511 EST 9.29 up 0.00001
 rc_N39254_s_at N39254 2512 EST 4.24 up 0.00478
 rc_N46423_at N46234 2521 EST 9.64 up 0.00027
 eukaryotic translation initiation factor 3, subunit 3 (gamma,
 rc_N47956_at N47956 2524 40kD) 6.34 up 0.00251
 rc_N49284_s_at N49284 2537 v-myb avian myeloblastosis viral oncogene homolog 11.82 up 0.01981
 rc_N49738_at N49738 2539 EST 3.81 up 0.02479
 rc_N50048_at N50048 2542 EST 4.08 up 0.00085
 rc_N51053_s_at N51053 2543 eukaryotic translation initiation factor 5 3.42 up 0.01326
 rc_N51342_at N51342 2545 EST 3.56 up 0.0001
 rc_N52168_at N52168 2551 EST 5.65 up 0.00003
 rc_N54841_at N54841 2572 EST 42.96 up 0.00002
 rc_N56935_s_at N56935 2575 EST 3.57 up 0.00282
 rc_N58463_at N58463 2580 PCTAIRE protein kinase 1 3.18 up 0.00649
 rc_N62126_at N62126 2589 EST 8.51 up 0.00016
 rc_N62675_s_at N62675 2594 DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 16 3.61 up 0.04034
 rc_N62819_at N62819 2595 EST 3.25 up 0.01137
 rc_N64616_at N64616 2611 EST 3.11 up 0.0074
 rc_N66139_s_at N66139 2615 neurochondrin

4.03 up 0.00118
 homolog of mouse quaking QKI (KHdomain RNA binding
 rc_N66624_at N66624 2618 protein) 6.25 up 0
 rc_N66951_at N66951 2621 EST 5.54 up 0.02442
 rc_N67205_at N67205 2625 EST 3.1 up 0.00626
 rc_N68038_f_at N68038 2632 phorbolin (similar to apolipoprotein B mRNA editing protein) 3.75 up 0.01041 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_N68385_f_at N68385 2635 ribosomal protein L13a 3.57 up 0.00417
 rc_N68921_at N68921 2639 EST 4.4 up 0.00989
 rc_N69252_f_at N69252 2647 ferritin, light polypeptide 5.33 up 0.01554
 rc_N69263_at N69263 2648 EST 7.47 up 0.00004
 rc_N70577_at N70577 2659 EST 3.07 up 0.01975
 rc_N70678_s_at N70678 2660 TAR (HIV) RNA-binding protein 1 4.2 up 0.00119
 rc_N70903_at N70903 2662 EST 4.41 up 0.0078
 rc_N71072_at N71072 2662 EST 5.57 up 0.03881
 rc_N71781_at N71781 2666 EST 7.01 up 0.02952
 solute carrier family 11 (proton-coupled divalent metal ion
 rc_N72116_s_at N72116 2668 transporter, member 2 9.01 up 0.00051
 rc_N73762_f_at N73762 2678 EST 6.65 up 0.0023
 rc_N73808_f_at N73808 2679 EST 8.46 up 0.01886
 rc_N73846_at N73846 2680 EST 3.27 up 0.00012
 rc_N77947_s_at N77947 2698 EST 5 up 0.00117
 rc_N80703_at N80703 2704 EST 6.06 up 0.00003
 rc_N89670_at N89670 2709 EST 4.26 up 0.00002
 rc_N89937_at N89937 2711 LIM domain only 7 3.6 up 0.00375
 rc_N90238_i_at N90238 2712 EST 3.06 up 0.00354
 rc_N91023_at N91023 2716 EST 3.87 up 0.00008
 amyloid beta (A4) precursor protein-binding, family A, member
 rc_N92775_at N92775 2723 3 (X11-like 2) 3.86 up 0.00577
 rc_N92915_at N92915 2724 brefeldin A-inhibited guanine nucleotide-exchange protein 1 3.1 up 0.00807
 rc_N92934_s_at N92934 2725 cysteine-rich protein 1 (intestinal) 35.52 up 0.002
 rc_N93105_f_at N93105 2728 EST 3.77 up 0.02195
 rc_N93798_at N93798 2738 protein tyrosine phosphatase type IVA, member 3 4.65 up 0.00118
 rc_N98464_s_at N98464 2744 EST 15.5 up 0.00004
 rc_N98758_f_at N98758 2745 EST 3.87 up 0.0074
 N99505_at N99505 2746 EST 3.6 up 0.4499
 rc_R02036_at R02036 2754 EST 8.01 up 0.01012 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_R06251_f_at R06251 2764 tumor protein D52-like 2 5.57 up 0.00037
 rc_R06254_f_at R06254 2765 tumor protein D52-like 2 4.64 up 0.00039
 rc_R06866_s_at R06866 2774 EST 5.18 up 0.00187
 rc_R06986_f_at R06986 2776 peptidylprolyl isomerase B (cylophilin B) 3.01 up 0.04418
 rc_R22565_at R22565 2800 EST 4.8 up 0.0424
 rc_R26706_s_at R26706 2803 EST 3.21 up 0.03858
 rc_R26744_at R26744 2804 midline 1 (Opitz/BBB syndrome) 4.32 up 0.00532
 rc_R27432_at R27432 2808 EST 3.62 up 0.00014
 UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase,
 rc_R28636_at R28636 2809 polypeptide 3 3.78 up 0.00765
 rc_R31107_at R31107 2812 EST 4.12 up 0.00003
 rc_R33498_s_at R33498 2820 EST 41.34 up 1.00001
 rc_R36947_s_at R36947 2825 calcium channel, voltage-dependent, beta 3 subunit 4.11 up 0.00006
 rc_r38076_s_at R38076 2828 EST 4.08 up 0.00374
 rc_R38239_at R38239 2830 EST 7.14 up 0.00249
 rc_R38280_at R38280 2831 BCS1 (yeast homolog)-like 3.68 up 0.0009
 rc_R38511_s_at R38511 2832 protein similar to E.coli yhdg and R. capsulatus nifR3 5.19 up 0.00015
 rc_R39119_s_at R39119 2834 KIAA1020 protein 4.69 up 0.00456
 rc_R40254_at R40254 2840 EST 5.82 up 0.00304
 rc_R43952_at R43952 2853 homeo box B5 4.11 up 0.04316
 rc_R44479_at R44479 2855 KIAA0552 gene product 4.14 up 0.0181
 rc_R44538_at R44538 2856 EST 5.73 up 0.01015
 rc_r45698_at R45698 2866 EST 3.01 up 0.04766
 rc_R45994_f_at R45994 2867 EST 7.81 up 0.0018
 rc_R48447_at R48447 2871 EST 7.75 up 0.00049
 rc_R48589_at R48589 2874 EST 4.95 up 0.01346
 rc_R49084_s_at R49084 2879 KIAA0770 protein 3.57 up 0.00447
 rc_R49216_at R49216 2880 EST 3.64 up 0.0004
 rc_R49395_s_at R49395 2881 EST 4.38 up 0.00112
 rc_R49476_at R49476 2883 EST 10.95 up 0.00014
 rc_R52161_at R52161 2893 EST 5.84 up 0.03253 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_R53109_f_at R53109 2899 dimethylarginine dimethylaminohydrolase 2 3.31 up 0.02389
 rc_R53109_r_at R53109 2899 dimethylarginine

dimethylaminohydrolase 2 3.22 up 0.00724
 rc_R54614_s_at R54614 2902 EST 3.24 up
 0.00526
 rc_R55470_at R55470 2904 EST 3.59 up 0.00515
 rc_R56095_s_at R56095 2906
 EST 8.16 up 0.00023
 R56678_at R56678 2908 EST 3.81 up 0.02242
 rc_R56880_at R56880
 2909 EST 6.82 up 0.02559
 rc_R58974_at R58974 2910 EST 4.95 up 0.00498

 rc_R59352_s_at R59352 2915 KIAA0296 gene product 4.19 up 0.00393
 rc_r61297_s_at R61297
 2920 eukaryotic translation initiation factor 3, subunit 6 (48kD) 6.42 up 0.00126
 R69700_at
 R69700 2943 EST 6.71 up 0.0021
 rc_R70005_at R70005 2944 EST 4.61 up 0.00037

 rc_R70801_s_at R70801 2950 EST 6.36 up 0.00563
 rc_R71082_s_at R71082 2951 programmed
 cell death 5 3.6 up 0.01338
 rc_R71395_at R71395 2952 EST 10.42 up 0.00422

 rc_R73565_at R73565 2959 EST 3.29 up 0.03489
 O-linked N-acetylglucosamine (GlcNAc)
 transferase (UDP-N-
 acetylglucosamine:polypeptide-N-acetylglucosaminyl
 rc_R76782_s_at
 R76782 2963 transferase) 5.83 up 0.01126
 rc_R77631_at R77631 2967 EST 3.43 up
 0.00006
 rc_R79580_at R79580 2970 EST 6.25 up 0.00593
 rc_R87989_at R87989 2979
 centrosome associated protein 3.64 up 0.00008
 rc_R91819_at R91819 2984 EST 8.95 up
 0.00009
 rc_R92994_s_at R92994 2990 matrix metalloproteinase 12 (macrophage elastase) 11.05
 up 0.00248
 rc_R95966_i_at R95966 2997 EST 11.22 up 0.00682
 rc_R96924_s_at R96924
 3001 EST 6.18 up 0.03417
 rc_R97759_at R97759 3006 serum/glucocorticoid regulated kinase
 5.99 up 0.00221
 S54005_s_at S54005 3020 thymosin, beta 10 7.03 up 0.00334
 S56151_s_at
 S56151 3021 milk fat globule-EGF factor 8 protein 4.59 up 0.0091
 S69272_s_at S69272 3028
 protease inhibitor 6 (placental thrombin inhibitor) 5.15 up 0.00003 Table 6A. Genes up regulated in
 metastatic tissue versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name
 Fold Change Direction Pvalue
 S73885_s_at S73885 3032 transcription factor AP-4 (activating
 enhancer-binding protein 4) 4.18 up 0.00005
 S78187_at S78187 3036 cell division cycle 25B 8.07
 up 0.00009
 s81914_at S81914 3038 immediate early response 3 5.46 up 0.01798

 rc_T03313_at T03313 3042 dyskeratosis congenita 1, dyskerin 9.63 up 0.00001
 rc_T03438_s_at
 T03438 3043 EST 8.18 up 0.00032
 rc_T03580_f_at T03580 3046 pyruvate kinase, muscle 24.91
 up 0.0001
 rc_T12599_f_at T12599 3056 ribosomal protein L21 3.54 up 0.01437

 rc_T15442_f_at T15442 3057 calpain, large polypeptide L1 5.01 up 0.00255
 rc_T15473_at
 T15473 3058 muscle specific gene 5.81 up 0.02404
 rc_T15477_at T15477 3059 EST 3.61 up
 0.00005
 rc_T15903_s_at T15903 3063 EST 3.23 up 0.01377
 rc_T16308_f_at T16308 3069
 EST 5.29 up 0.00119
 rc_T16983_s_at T16983 3074 cleavage and polyadenylation specific factor
 4, 30kD subunit 5.23 up 0.00075
 rc_T23465_at T23465 3081 EST 4.4 up 0.017

 rc_T23490_i_at T23490 3082 EST 11.86 up 0.03242
 rc_T23516_f_at T23516 3083 3-
 phosphoglycerate dehydrogenase 5.38 up 0.00001
 rc_T24068_s_at T24068 3088 EST 15.26 up
 0.00046
 rc_T25725_at T25725 3091 EST 3.26 up 0.00099
 rc_T26366_f_at T26366 3093
 EST 30.43 up 0.00153
 rc_T26471_at T26471 3094 EST 4.62 up 0.01091
 protein
 phosphatase 2 (formerly 2A), regulatory subunit A (PR
 rc_T26513_i_at T26513 3095 65), alpha
 isoform 5.07 up 0.0016
 rc_T26574_s_at T26574 3096 catenin (cadherin-associated protein), delta
 1 3.17 up 0.00828
 rc_T30193_s_at T30193 3098 protease, serine, 8 (prostasin) 8.39 up
 0.0043
 rc_T32072_s_at T32072 3102 EST 5.95 up 0.00029
 rc_T32108_at T32108 3103
 EST 6.96 up 0.00723
 rc_T33489_s_at T33489 3105 EST 8.04 up 0.00469
 rc_T33508_s_at
 T33508 3106 phosphatidylinositol-4-phosphate 5-kinase, type II, beta 3.31 up 0.00416 Table 6A. Genes
 up regulated in metastatic tissue versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known
 Gene Name Fold Change Direction Pvalue
 T35341_s_at T35341 3112 EST 4.73 up 0.00057

 T35725_s_at T35725 3113 EST 3.4 up 0.00149
 rc_T40849_s_at T40849 3116 maternal G10
 transcript 4.11 up 0.00449
 rc_T47032_s_at T47032 3124 partner of RAC1 (arfaptin 2) 3.27 up
 0.00503
 rc_T47325_s_at T47325 3125 EST 5.63 up 0.01015
 rc_T47601_at T47601 3126
 EST 4.05 up 0.00878
 ceroid-lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-

 rc_T47969_s_at T47969 3128 Vogt disease) 3.03 up 0.03452
 eukaryotic translation initiation
 factor 3, subunit 3 (gamma,
 T48195_s_at T48195 3131 40kD) 3.75 up 0.00012

 rc_T48293_f_at T48293 3133 EST 3.55 up 0.01355
 rc_T53404_at T53404 3143 EST 10.68 up

0.00582
 rc_T55004_s_at T55004 3146 EST 4.83 up 0.00156
 rc_T55196_at T55196 3147 EST 4.04 up 0.00012
 rc_T58153_s_at T58153 3154 heat shock 105kD 3.08 up 0.01317
 rc_T58607_at T58607 3155 EST 3.52 up 0.4102
 rc_T59161_s_at T59161 3159 thymosin, beta 10 3.41 up 0.01885
 rc_T59668_s_at T59668 3160 lysyl oxidase 3.28 up 0.00588
 rc_T66935_at T66935 3179 EST 3.97 up 0.00188
 rc_T7733_s_at T77733 3219 tubulin, gamma 1 4.42 up 0.00049
 rc_T78922_s_at T78922 3222 stem cell growth factor; lymphocyte secreted C-type lectin 3.42 up 0.02419
 rc_T91116_at T91116 3252 EST 4.01 up 0.02721
 rc_T92935_at T92935 3255 EST 3.48 up 0.03578
 rc_T95057_f_at T95057 3259 EST 10.39 up 0.00003
 rc_T98284_at T98284 3268 EST 4.47 up 0.00054
 U01062_at U01062 3273 inositol 1,4,5-triphosphate receptor, type 3 7.41 up 0
 U01147_at U01147 3275 active BCR-related gene 3.22 up 0.00103
 non-Pou domain-containing octamer (ATGCAAAT) binding
 U02493_at U02493 3279 protein 3.04 up 0.0019 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 U03891_at U03891 3283 phorbolin (similar to apolipoprotein B mRNA editing protein) 3 up 0.00065
 U04313_at U04313 3284 protease inhibitor 5 (maspin) 4.54 up 0.02986
 U05875_at U05875 3286 interferon gamma receptor 2 (interferon gamma transducer 1) 3.09 up 0.00549
 U07969_s_at U07969 3289 cadherin 17, LI cadherin (liver-intestine) 10.78 up 0.02002
 U09117_at U09117 3294 phospholipase C, delta 1 7.96 up 0.00001
 U09564_at U09564 3295 SFRS protein kinase 1 3.79 up 0.00765
 U09770_at U09770 3296 cysteine-rich protein 1 (intestinal) 13.03 up 0.0072
 U11861_at U11861 3298 maternal G10 transcript 3.8 up 0.00001
 U12404_at U12404 3299 ribosomal protein L10a 4.18 up 0.00004
 U12465_at U12465 3300 ribosomal protein L35 4.69 up 0.00001
 U14968_at U14968 3303 ribosomal protein L27a 4.01 up 0.00003
 U14969_at U14969 3304 ribosomal protein L28 4.63 up 0.00004
 U14970_at U14970 3305 ribosomal protein S5 3.45 up 0.00915
 U14971_at U14971 3306 ribosomal protein S9 3.93 up 0.00026
 U14972_at U14972 3307 ribosomal protein S10 5.24 up 0.00077
 U14973_at U14973 3308 ribosomal protein S29 3.1 up 0.00028
 U15008_at U15008 3309 small nuclear ribonucleoprotein D2 polypeptide (16.5kd) 4.9 up 0.00396
 U17077_at U17077 3314 BENE protein 4.98 up 0.00366
 laminin, beta 3 (nicein (125kD), kalinin (140kD), BM600
 U17760_ma1_at U17760 3315 (125kD)) 3.54 up 0.01853
 U20499_at U20499 3321 sulfotransferase family 1A, phenol-preferring, member 3 5.5 up 0.00299
 secreted phosphoprotein 1 (osteopontin, bone sialoprotein I,
 U20758_ma1_at U20758 3323 early T-lymphocyte activation 1) 6.12 up 0.03448
 epithelial protein up-regulated in carcinoma, membrane
 U21049_at U21049 3325 associated protein 17 7.53 up 0.01667
 U22376_cds2_s_at U22376 3328 v-myb avian myeloblastosis viral oncogene homolog 3.34 up 0.03416
 U25789_at U25789 3334 ribosomal protein L21 4.37 up 0.00045 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 U26726_at U26726 3336 hydroxysteroid (11-beta) dehydrogenase 2 3.45 up 0.02342
 fucosyltransferase 3 (galactoside 3(4)-L-flucosyltransferase,
 U27328_s_at U27328 3338 Lewis blood group included) 3.05 up 0.03224
 U31556_at U31556 3346 E2F transcription factor 5, p130-binding 4.14 up 0.01157
 U33286_at U33286 3349 chromosome segregation 1 (yeast homolog)-like 3.39 up 0.00939
 solute carrier family 6 (neurotransmitter transporter, creatine),
 U36341_ma1_at U36341 3351 member 8 3.05 up 0.02622
 U37689_at U37689 3356 polymerase (RNA) II (DNA directed) polypeptide H 3.65 up 0.00044
 potassium voltage-gated channel, KQT-like subfamily, member
 U40990_at U40990 3359 1 3.18 up 0.00093
 U42408_at U42408 3361 laminin 1 6.8 up 0.00305
 U43901_ma1_s_at U43901 3362 laminin receptor 1 (67kD, ribosomal protein SA) 3.11 up 0.03145
 U46692_ma1_at U46692 3367 cystatin B (stein B) 5.54 up 0.00016
 U47025_s_at U47025 3368 phosphorylase, glycogen; brain 8.52 up 0.00134
 U48705_ma1-s_at U48705 3370 discoidin domain receptor family, member 1 5.94 up 0.01323
 U51095_at U51095 3382 caudal type homeo box transcription factor 1 4.76 up 0.02664
 U51478_at U51478 3385 ATPase, Na⁺/K⁺ transporting, beta 3 polypeptide 5.75 up 0.00007
 solute carrier family 1 (neutral amino acid transporter), member
 U53347_at

U53347 3389 5 3.81 up 0.00273
 U53830_at U53830 3391 interferon regulatory factor 7 3.94 up
 0.03147
 U58682_at U58682 3396 ribosomal protein S28 6.09 up 0.00001
 U62392_at
 U62392 3403 zinc finger protein 193 3.18 up 0.00269
 U62962_at U62962 3404 eukaryotic
 translation initiation factor 3, subunit 6 (48kD) 4.05 up 0.0047
 U67171_at U67171 3409
 selenoprotein W, 1 3.08 up 0.0047
 U73379_at U73379 3418 ubiquitin carrier protein E2-C 8.32
 up 0.00101
 U73843_at U73843 3421 E74-like factor 3 (ets domain transcription factor) 5.75 up
 0.00017
 U75285_ma1_at U75285 3422 apoptosis inhibitor 4 (survivin) 4.46 up 0.02212

 U76366_s_at U76366 3424 Treacher Collins-Franceschetti syndrome 1 3.44 up 0.00021

 U78027_ma3_at U78027 3429 EST 4.15 up 0.00295
 U78095_at U78095 3430 serine protease
 inhibitor, Kunitz type, 2 18.85 up 0 Table 6A. Genes up regulated in metastatic tissue versus normal
 sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction
 Pvalue
 U78525_at U78525 3432 eukaryotic translation initiation factor 3, subunit 9 (eta, 116kD)
 4.68 up 0.00132
 U78556_at U78556 3433 cisplatin resistance associated 5.77 up 0.00241

 U79266_at U79266 3434 protein predicted by clone 23627 3.49 up 0.00004
 U79725_at U79725
 3438 glycoprotein A33 (transmembrane) 8.57 up 0.00299
 U83246_at U83246 3443 copine I 3.57
 up 0.01672
 U84720_at U84720 3446 RAE1 (RNA export 1, S:pombe) homolog 3.37 up
 0.03586
 U85773_at U85773 3449 phosphomannomutase 2 3.94 up 0.00288
 U86409_at
 U86409 3450 EST 3.38 up 0.00003
 U89606_at U89606 3452 pyridoxal (pyridoxine, vitamin B6)
 kinase 3.57 up 0.00322
 U90549_at U90549 3456 high-mobility group (nonhistone chromosomal)
 protein 17-like 3 3.2 up 0.0401
 U90913_at U90913 3459 Tax interaction protein 1 4.35 up
 0.00159
 U93205_at U93205 3461 chloride intracellular channel 1 6.14 up 0.00058

 U93686_at U93686 3463 polymerase (RNA) III (DNA directed) (32kD) 3.5 up 0.01235

 rc_W02041_at W02041 3466 EST 4.83 up 0.00158
 rc_W20391_s_at W20391 3479 kinesin-like 2
 3.98 up 0.01788
 W28362_at W28362 3488 KIAA0974 protein 3.98 up 0.00626

 rc_W31382_at W31382 3495 EST 4 up 0.00058
 rc_W37680_at W37680 3503 EST 3.55 up
 0.01036
 rc_W37937_at W37937 EST 3.07 up 0.00776
 myeloid/lymphoid or mixed-lineage
 leukemia (trithorax
 rc_W38044_s_at W38044 (Drosophila) homolog); translocated to, 7 7.28 up
 0.03105
 W39183_s_at W39183 3508 KIAA0601 protein 3.66 up 0.00018
 rc_W42627_f_at
 W42627 3511 EST 3.56 up 0.00198
 rc_W42957_at W42957 3516 calmodulin 2 (phosphorylase
 kinase, delta) 15.22 up 0.00007
 rc_W44557_at W44557 3518 chromosome 1 open reading frame 2
 4.32 up 0.00128
 rc_W44733_at W44733 3519 EST 3.02 up 0.00097
 rc_W45487_s_at
 W45487 3524 dynamin 2 4.2 up 0.00325
 rc_W49574_at W49574 3538 EST 5.97 up
 0.00045
 rc_W49661_s_at W49661 3539 FK506-binding protein 9 (63 kD) 3.01 up 0.02259 Table
 6A. Genes up regulated in metastatic tissue versus normal sample set 2.
 <P>Affy ID Genbank Seq
 ID Known Gene Name Fold Change Direction Pvalue
 W52858_at W52858 3545
 DKFZP564F0522 protein 4.38 up 0.00088
 rc_W60486_at W60486 3558 EST 4.29 up
 0.00964
 rc_W67251_s_at W67251 3570 EST 6.13 up 0.01463
 rc_W70336_at W70336 3579
 EST 3.65 up 0.01776
 rc_W72276_at W72276 3583 EST 27.39 up 0.00183
 protein tyrosine
 phosphatase, receptor type, f polypeptide
 rc_W72861_at W72861 3586 (PTPRF), interacting
 protein (liprin), alpha 3 3.0 up 0.00055
 rc_W73189_at W73189 3589 EphB2 3.69 up
 0.02909
 rc_W73914_at W73914 3595 EST 3.5 up 0.04782
 rc_W74233_s_at W74233 3597
 related RAS viral (r-ras) oncogene homolog 6.02 up 0.01815
 W76097_at W76097 3599 EST 3.83
 up 0.00001
 rc_W78057_at W78057 3600 EST 9.06 up 0.0034
 rc_W80730_at W80730 3607
 EST 6.59 up 0.00425
 rc_W80763_at W80763 3608 EST 3.83 up 0.01319
 rc_W81375_at
 W81375 3613 EST 3.58 up 0.00322
 rc_W81540_at W81540 3614 serine/threonine kinase 24
 (Ste20, yeast homolog) 6.72 up 0.00164
 rc_W90146_f_at W90146 3644 EST 6.23 up
 0.01558
 rc_W92207_at W92207 3651 EST 6.77 up 0.00002
 rc_W92449_at W92449 3652
 EST 31.67 up 0.00011
 rc_W92608_s_at W92608 3653 BAI1-associated protein 3 5.12 up
 0.00075
 rc_W93726_s_at W93726 3656 protease inhibitor 5 (maspin) 16.48 up 0.00014

 rc_W93943_at W93943 3657 EST 4.3 up 0.00296
 W95348_at W95348 3663 HSPC113 protein
 10.89 up 0.01065
 rc_W95477_at W95477 3664 EST 26.51 up 0.00161
 X03342_at X03342

3675 ribosomal protein L32 4.09 up 0.00008
 AFFX-CreX-5_at x03453 3677 EST 3.03 up 0.0025
 X04347_s_at X04347 3680 heterogeneous nuclear ribonucleoprotein A1 7.26 up 0.00018
 X05610_at X05610 3685 collagen, type IV, alpha 2 3.58 up 0.01351
 X06617_at X06617 3687 ribosomal protein S11 4.32 up 0.0002
 X07820_at X07820 3695 matrix metalloproteinase 10 (stromelysin 2) 3.49 up 0.00689 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 X12447_at X12447 3696 aldolase A, fructose-bisphosphate 10.52 up 0.00038
 X13956_at X13956 3701 EST 3.2 up 0.00321
 X14850_at X14850 3706 H2A histone family, member X 4.11 up 0.0001
 X15940_at X15940 3709 ribosomal protein L31 4.45 up 0.0004
 X17093_at X17093 3716b EST 4.82 up 0.00176
 X17206_at X17206 3718 ribosomal protein S2 5.14 up 0
 X17567_s_at X17567 3719 small nuclear ribonucleoprotein polypeptides B and B1 3.6 up 0.00586
 X51466_at X51466 3720 eukaryotic translation elongation factor 2 3.25 up 0.00019
 X51521_at X51521 3721 villin 2 (ezrin) 3.89 up 0.0001
 X52851_mal_at X52851 3725 EST 3.38 up 0.0001
 X52966_at X52966 3726 ribosomal protein L35a 3.93 up 0.00217
 X53331_at X53331 3727 matrix Gla protein 3.66 up 0.04038
 X54667_s_at X54667 3731 cystatin S, cystatin SN 8.53 up 0.00059
 X55715_at X55715 3735 ribosomal protein S3 3.72 up 0.00755
 X55954_at X55954 3736 ribosomal protein L23 3.81 up 0.00025
 X56494_at X56494 3738 pyruvate kinase, muscle 22.97 up 0.00001
 X56932_at X56932 3740 ribosomal protein L13a 3.26 up 0
 X56997_mal_at X56997 3741 ubiquitin A-52 residue ribosomal protein fusion product 1 3.18 up 0.0006
 X57348_s_at X57348 3744 stratifin 12.53 up 0.0013
 X62535_at X62535 3756 diacylglycerol kinase, alpha (80kD) 4.72 up 0.00315
 X62691_at X62691 3757 ribosomal protein S15a 4.09 up 0.00004
 X63627_at X63627 3761 ribosomal protein L19 3.17 up 0.02488
 X63629_at X63629 3762 cadherin 3, P-cadherin (placental) 3.02 up 0.01654
 X64364_at X64364 3764 basigin 6.45 up 0.00041
 X64707_at X64707 3765 ribosomal protein L13 4.28 up 0.00257
 X65614_at X65614 3767 S100 Calcium-binding protein P 12.2 up 0.00056
 X66364_at X66364 3770 cyclin-dependent kinase 5 3.55 up 0.02824
 proteasome (prosome, macropain) subunit, beta type, 9 (large
 X66401_cds1_at X66401 3771 multifunctional protease 2) 3.68 up 0.01385
 X66899_at X66899 3772 Ewing sarcoma breakpoint region 1 4.72 up 0.00011 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 X67247_mal_at X67247 3774 mitogenactivated protein kinase kinase kinase kinase 3 3.48 up 0.00012
 X67325_25 X67325 3775 interferon, alpha-inducible protein 27 9.67 up 0.03245
 X68314_at X68314 3778 glutathione peroxidase 2 (gastrointestinal) 14.4 up 0.00222
 X68688_mal_s_at X68688 3780 zinc finger protein 33a (KOX 31) 4.7 up 0.00062
 X68668_mal_s_at X68668 3780 zinc finger protein 33a (KOX 31) 3.62 up 0.00319
 X69150_at X69150 3782 ribosomal protein S18 4.5 up 0.00003
 X69391_at X69391 3783 ribosomal protein L6 3.18 up 0.00004
 CD47 antigen (Rh-related antigen, integrin-associated signal
 X69398_at X69398 3784 transducer) 3.68 up 0.02332
 X69654_at X69654 3785 ribosomal protein S26 3.11 up 0.02683
 ATP synthase, H⁺ transporting, mitochondrial F0 complex,
 X69908_mal_at X69908 3786 subunit c (subunit 9), isoform 2 3.73 up 0.00685
 macrophage stimulating 1 receptor (c-met-related tyrosine
 X70040_at X70040 3788 kinase) 4 up 0.00402
 X74929_s_at X74929 3792 keratin 8 4.73 up 0.00018
 X76180_at X76180 3795 sodium channel, nonvoltage-gated 1 alpha 11.68 up 0
 X77588_s_at X77588 3799 N-acetyltransferase, homolog of S. cerevisiae ARD1 3.91 up 0.0221
 X78687_at X78687 3800 sialidase 1 (lysosomal sialidase) 3.18 up 0.031
 X79234_at X79234 3803 ribosomal protein L11 3.59 up 0.00051
 X79882_at X79882 3805 lung resistance-related protein 6.71 up 0.0362
 X8198_at X8198 3807 steroidogenic acute regulatory protein related 3.03 up 0.00044
 X80822_at X80822 3808 ribosomal protein L18a 4.13 up 0.0006
 X80822_f_at X80822 3808 ribosomal protein L18a 3.08 up 0.02481
 X80909_at X80909 3809 nascent-polypeptide-associated complex alpha polypeptide 3.84 up 0.00399
 X833228_at X833228 3810 cadherin 17, LI cadherin (liver-Intestine) 10.58 up 0.02147
 X89960_at X89960 3818 EST 9.87 up 0
 high-mobility group (nonhistone

chromosomal) protein isoform I0-
 X92518_s_at X92518 3825 C 3.12 up 0.00638
 X93036_at X93036 3830 FXFD domain-containing ion transport regulator 3 42.36 up 0.00167 Table 6A. Genes up regulated in metastatic tissue versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction pvalue
 X95404_at X95404 3834 cofilin 1 (non-muscle) 3.18 up 0.00104
 X98482_r_at X98482 3841 EST 5.03 up 0.00002
 X99133_at X99133 3842 lipocalin 2 (oncogene 24p3) 6.27 up 0.0453
 Y00503_at Y00503 3849 keratin 19 14.19 up 0.00217
 Y00705_at Y00705 3850 serine protease inhibitor, Kazal type 1 9.83 up 0.03697
 Y10807_s_at Y10807 3860 HMT1 (hnRNP methyltransferase, *S. cerevisiae*)-like 2 4.28 up 0.00124
 Z23090_at Z23090 3868 heat shock 27kD protein 1 7.67 up 0.00008
 Z24727_at Z24727 3871 tropomyosin 1 (alpha) 4.47 up 0.00121
 nuclear factor of kappa light polypeptide gene enhancer in B-
 Z25749_rna1_at Z25749 3872 cells inhibitor-like 2 4.41 up 0.00031
 Z26876_at Z26876 3874 ribosomal protein L38 4.43 up 0.00022
 Z28407_at Z28407 3876 ribosomal protein L8 6.3 up 0.00004
 Z30643_at Z30643 3879 chloride channel Ka 3.86 up 0.00204
 rc_Z38150_s_at Z38150 3883 EST 3.06 up 0.00049
 rc_Z38266_at Z38266 3886 EST 6.58 up 0.01909
 rc_Z38729_at Z38729 3894 EST 3.13 up 0.04514
 rc_Z38909_at Z38909 3897 EST 3.55 up 0.03195
 rc_Z39079_at Z39079 3900 KIAA1058 protein 4.08 up 0.01781
 rc_Z39191_at Z39191 3901 EST 8.84 up 0.00011
 rc_Z39200_at Z39200 3902 EST 3.29 up 0.00586
 rc_Z39429_at Z39429 3906 EST 7.84 up 0.00045
 rc_Z39930_f_at Z39930 3914 EST 3.07 up 0.00002
 rc_Z40583_f_at Z40583 3922 EST 4.24 up 0.02375
 rc_Z40898_at Z40898 3925 EST 3.71 up 0.01168
 rc_Z40945_at Z40945 3927 trinucleotide repeat containing 15 7.82 up 0.00007
 rc_Z41103_at Z41103 3929 trinucleotide repeat containing 15 3.83 up 0.00444
 rc_Z41740_s_at Z41740 3935 EST 6.76 up 0.00049
 rc_Z41798_s_at Z41798 3937 EST 6.7 up 0.00073
 Z68228_s_at Z68228 3947 junction plakoglobin 3.3 up 0.0237
 Z74615_at Z74615 3949 collagen, type I, alpha 1 10.47 up 0.00064
 Z74616_s_at Z74616 3950 collagen, type I, alpha 2 4.83 up 0.02364 Table 6B. Down regulated in metastatic cancer sversus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_AA001603_at AA001603 3 EST 4.31 down 0.00883
 rc_AA001604_at AA001604 4 EST 3.33 down 0.0215
 AA004231_at AA004231 7 EST 3.16 down 0.03067
 rc_AA004521_at AA004521 8 prostate cancer overexpressed gene 1 8.03 down 0.00027
 rc_AA004905_at AA004905 11 KIAA0937 protein 4.63 down 0.00082
 rc_AA005202_at AA005202 12 retinol-binding protein 4, interstitial 3.18 down 0.00106
 rc_AA005358_at AA005358 14 EST 5.2 down 0.00138
 rc_AA007629_at AA007629 19 EST 8.01 down 0.00001
 rc_AA009719_at AA009719 20 peroxisomal membrane protein 2 (22kD) 47.12 down 0.00008
 rc_AA010205_at AA010205 23 EST 7.41 down 0
 rc_AA010360_at AA010360 24 EST 6.55 down 0.00027
 rc_AA010530_at AA010530 25 EST 3.74 down 0.0481
 rc_AA010619_at AA010619 27 EST 8.55 down 0.00057
 AA010750_at AA010750 28 calmodulin 1 (phosphorylase kinase, delta) 10.22 down 0.00959
 rc_AA015768_at AA015768 34 EST 15.3 down 0.00008
 rc_AA017146_at AA017146 36 EST 10.1 down 0.00052
 rc_AA017192_at AA017192 37 EST 3.43 down 0.04865
 rc_AA018867_at AA018867 39 EST 42.87 down 0.00002
 rc_AA021623_s_at AA021623 43 insulin induced gene 1 11.71 down 0.00094
 rc_AA025930_at AA025930 52 EST 3.59 down 0.00372
 rc_AA031543_s_at AA031543 68 translocation protein 1 5.92 down 0.00405
 AA031548_at AA031548 68 cell division cycle 42 (GTP-binding protein, 25kD) 3.65 down 0.03029
 rc_AA032005_at AA032005 71 EST 5.3 down 0.01202
 AA032048_at AA032048 72 EST 5.45 down 0.00383
 rc_AA032250_at AA032250 73 EST 3.56 down 0.0009
 rc_AA034030_at AA034030 75 methylmalonyl Coenzyme A mutase 14.32 down 0.00004
 rc_AA035245_s_at AA035245 79 aldehyde oxidase 1 69.82 down 0.00117
 rc_AA035457_at AA035457 80 EST 10.06 down 0.00085
 rc_AA035638_at AA035638 82 EST 9.91 down 0.00541
 rc_AA036662_s_at AA036662 83 EST 4.16 down 0.00235
 rc_AA037357_f_at AA037357 85 EST 3.53 down 0.02129 Table 6B. Down regulated in metastatic cancer sversus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_AA039335_s_at

AA039335 89 coagulation factor XII (Hageman factor) 32 down 0.0029
 rc_AA039616_at
AA039616 90 eST 9.36 down 0.00009
 AA039806_at AA039806 91 msh (Drosophila) homeo box
homolog 1 3.53 down 0.00114
 rc_AA040087_at AA040087 92 EST 4.13 down 0.00123

rc_AA040270_at AA040270 93 EST 3.03 down 0.01367
 rc_AA040291_at AA040291 94
KIAA0669 gene product 3.55 down 0.00308
 rc_AA043501_at AA043501 98 v-maf
musculoaponeurotic fibrosarcoma (avian) 3.81 down 0.01304
 AA044622_at AA044622 103 EST
3.62 down 0.03789
 AA044755_s_at AA044755 104 EST 6.7 down 0.01228
 AA044842_at
AA044842 105 Autosomal Highly Conserved protein 5.231 down 0.0009
 AA045870_at
AA045870 108 EST 5.93 down 0.00017
 rc_AA046457_at AA046457 111 EST 3.2 down
0.00513
 AA046674_at AA046674 112 EST 5.17 down 0.02561
 rc_AA046747_at
AA046747 114 EST 4.82 down 0.00022
 AA046840_at AA046840 115 CCAAT/enhancer binding
protein (C/EBP). delta 3.79 down 0.03319
 AA047151_at AA047151 116 EST 7.13 down
0.00007
 rc_AA047187_at AA047187 117 EST 3.04 down 0.04306
 rc_AA047290_at
AA047290 118 EST 3.39 down 0.00024
 rc_AA052980_at AA052980 122 EST 4.52 down
0.023
 rc_AA055992_at AA055992 136 calumenin 3.51 down 0.0064
 AA056170_at
AA056170 137 EST 3.82 down 0.0083
 rc_AA056247_at AA056247 138 EST 3.48 down
0.03277
 rc_AA056482_at AA056482 141 EST 4.82 down 0.00199
 rc_AA057678_at
AA057678 143 EST 6.88 down 0.00078
 AA059489_at AA059489 145 RGC32 protein 3.74 down
0.00734
 rc_AA062744_at AA062744 147 EST 3.31 down 0.01909
 rc_AA065173_at
AA065173 148 EST 4.08 down 0.00377
 rc_AA069456_at AA069456 149 KIAA0438 gene
product 3.47 down 0.02718
 rc_AA069768_s_at AA069768 151 hevin 4.62 down 0.00202

AA070090_at AA070090 152 EST 3.24 down 0.00804
 rc_AA070091_at AA070091 153 EST 5
down 0 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID
Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_AA074885_at AA074885
161 macrophage receptor with collagenous structure 11.05 down 0.00786
 rc_AA074891_at
AA074891 162 EST 3.12 down 0.01897
 rc_AA076238_at AA076238 168 EST 3.23 down
0.00395
 rc_AA076249_at AA076249 169 TST 3.78 down 0.00029
 rc_AA076326_at
AA076326 170 SEC14 (S. Cerevisiae)-like 2 10.88 down 0.00616
 solute carrier family 25
(mitochondrial carrier;
 rc_AA079758_f_at AA079758 174 citrate transporter), member 1 7.83
down 0.00359
 rc_AA083812_at AA083812 175 DKFZP566F 123 protein 9.11 down
0.00167
 rc_AA084408_at AA084408 179 EST 4.05 down 0.00864
 rc_AA084668_at
AA084668 180 ubiquitin-like 3 3.19 down 0.0419
 rc_AA085987_s_at AA085987 183 UDP
glycosyltransferase 1 40.87 down 0.00004
 rc_AA086201_at AA086201 185 EST 5.8 down
0.00012
 rc_AA088698_at AA088698 188 EST 3.23 down 0.02543
 AA090257_at
AA090257 190 superoxide dismutase 2, mitochondrial 11.72 down 0.02072
 AA090434_at
AA090434 191 diaphanous (Drosophila, homolog) 1 4.61 down 0.01704
 AA090439_at
AA090439 192 ribosomal protein S6 5.58 down 0.00501
 AA092596_at AA092596 197 bone
morphogenetic protein 6 3.46 down 0.02532
 AA092716_at AA092716 198 HLA-B associated
transcript-3 13.97 down 0.0009
 AA093923_at AA093923 200 EST 3.82 down 0.03924

AA094507_s_at AA094507 201 EST 3.52 down 0.04783
 AA094999_at AA094999 204 zinc
finger protein 216 5.12 down 0.0257
 rc_AA099225_at AA099225 206 EST 7.33 down
0.00062
 AA099391_s_at AA099391 207 myosin, light polypeptide kinase 9.07 down
0.00003
 rc_AA099589_s_at AA099589 210 GDP dissociation inhibitor 2 3.7 down 0.04069

rc_AA101055_s_at AA101055 213 leptin receptor 3.14 down 0.0071
 rc_AA101235_at
AA101235 214 EST 8.46 down 0.00822
 rc_AA101632_at AA101632 217 EST 4.19 down
0.00023
 rc_AA112101_f_at AA112101 222 EST 8.5 down 0.00004
 rc_AA112209_s_at
AA112209 223 acyl-Coenzyme A dehydrogenase, long chain 3.37 down 0.00084
 UDP-N-
acetylglucosamine pyrophosphorylase 1;
 AA114949_at AA114949 228 Sperm associated antigen
2 5.12 down 0.01028 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.

<P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_AA121140_at
AA121140 235 EST 3.33 down 0.00058
 rc_AA122345_f_at AA122345 238 glutamate

dehydrogenase 1 16.53 down 0.00004
 rc_AA125831_r_at AA125831 241 myosin, light
 polypeptide kinase 8.18 down 0.00039
 rc_AA125856_at AA125856 242 EST 3.17 down
 0.01545
 rc_AA125861_at AA125861 243 EST 3.69 down 0.01547
 rc_AA126059_at
 AA126059 246 EST 3.08 down 0.00706
 rc_AA126722_s_at AA126722 251 O-6-methylguanine-
 DNA methyltransferase 8.26 down 0.002
 rc_AA127444_at AA127444 252 EST 3.56 down
 0.0291
 rc_AA127514_at AA127514 253 EST 3.4 down 0.00045
 rc_AA133215_at
 AA132215 277 calcitonin receptor-like receptor activity modifying 4.55 down 0.02092

 rc_AA133296_at AA133296 278 EST 4.23 down 0.00041
 rc_AA133439_at AA133439 279 EST
 4.07 down 0.00022
 rc_AA134549_at AA134549 288 EST 3.36 down 0.03438

 rc_AA135558_s_at AA135558 293 peptidase D 4.17 down 0.0068
 rc_AA135958_at AA135958
 296 EST 4.02 down 0.00012
 rc_AA136079_at AA136079 297 EST 4.26 down 0.0057

 rc_AA142849_at AA142849 306 EST 7.59 down 0.00804
 AA143019_at AA143019 309 EST
 6.75 down 0.00109
 rc_AA147646_s_at AA147646 317 DKFZP586A0522 protein 21.82 down
 0
 rc_AA148480_s_at AA148480 318 flavin containing monooxygenase 5 19.64 down 0

 rc_AA148923_at AA148923 321 decidal protein induced by progesterone 13.2 down 0.00257

 rc_AA149253_at AA149253 323 EST 5.12 down 0.00863
 rc_AA150776_at AA150776 330 EST
 10.45 down 0.00015
 rc_AA150891_at AA150891 331 EST 4.22 down 0.01692

 rc_AA151210_at AA151210 333 EST 4.61 down 0.00008
 rc_AA151676_at AA151676 337
 peptidyl arginine deiminase, type II 4.01 down 0.00911
 rc_AA156336_at AA156336 341 nuclear
 receptor co-repressor 1 3.69 down 0.01276
 4-nitrophenylphosphatase domain and non-
 rc_AA156656_at AA156656 344 neuronal SNAP25-like 1 15.01 down 0.01387
 rc_AA157112_at
 AA157112 345 EST 3.94 down 0.02571
 AA157520_at AA157520 347 EST 3.18 down 0.00516
 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank
 Seq ID Known Gene Name Fold Change Direction Pvalue
 aldo-keto reductase family 7, member
 A2
 rc_AA157799_at AA157799 348 (aflatoxin aldehyde reductase) 5.96 down 0

 rc_AA164586_s_at AA164586 359 estrogen receptor 1 5.8 down 0.0182
 rc_AA167565_at
 AA167565 362 EST 8.08 down 0.00046
 rc_AA171694_at AA171694 366 ceruloplasmin
 (ferroxidase) 21.23 down 0.00179
 rc_AA172372_at AA172372 370 EST 6.48 down
 0.00344
 rc_AA176233_at AA176233 376 EST 11.44 down 0.01856
 rc_AA179004_at
 AA179004 377 EST 14.34 down 0.00008
 rc_AA179387_at AA179387 379 DKFZP434N126
 protein 3.7 down 0.01588
 rc_AA180356_at AA180356 382 EST 3.16 down 0.00917

 rc_AA182030_at AA182030 387 EST 8.32 down 0.00018
 rc_AA182568_at AA182568 388
 STAT induced STAT inhibitor-2 10.92 down 0.00099
 AA188921_at AA188921 393 similar to
 Caenorhabditis elegans protein 4.05 down 0.004
 rc_AA190816_at AA190816 398 EST 4.1 down
 0.00037
 rc_AA191014_at AA191014 396 EST 5.07 down 0.01455
 protein phosphatase 2
 (formerly 2A), regulatory
 rc_AA191310_s_at AA191310 397 subunit A (PR 65), beta isoform
 7.28 down 0
 rc_AA191488_s_at AA191488 398 solute carrier family 31 (copper transporters),
 3.19 down 0.00013
 rc_AA191647_at AA191647 399 ceruloplasmin (ferroxidase) 4.05 down
 0.00029
 rc_AA193204_at AA193204 402 Arg/Abl-interacting protein ArgBP2 8.98 down
 0.00861
 rc_AA193223_at AA193223 403 EST 4.2 down 0.02416
 AA193297_at AA193297
 404 EST 4.37 down 0.04676
 rc_AA194075_f_at AA194075 406 nuclear receptor coactivator 4
 4.69 down 0.00862
 AA194146_at AA194146 407 EST 3.53 down 0.000352

 rc_AA194833_at AA194833 411 claudin 1 11.45 down 0.00034
 rc_AA194997_s_at AA194997
 412 EST 16.12 down 0.00103
 rc_AA195656_at AA195656 418 KIAA0977 protein 15.29 down
 0.00817
 rc_AA195657_at AA195657 419 EST 6.44 down 0.00016
 rc_AA196287_at
 AA196287 420 EST 15.07 down 0.00001
 intercellular adhesion molecule 1 (CD54), human

 rc_AA197311_s_at AA197311 1422 rhinovirus receptor 6.07 down 0.00053 Table 6B. Down regulated in
 metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name
 Fold Change Direction Pvalue
 FERM, RhoGEF (ARHGEF) and pleckstrin
 AA203222_at
 AA203222 424 domain protein 1 (chondrocyte-derived) 4.21 down 0.00745
 rc_AA205724_at
 AA205724 426 EST 6.73 down 0.00027
 rc_AA207123_at AA207123 430 immunoglobulin

superfamily, member 3 3.16 down 0.00328
 rc_AA210850_at AA210850 431 EST 4.97 down 0.00735
 rc_AA211388_at AA211388 433 EST 4.56 down 0.02703
 rc_AA214542_at AA214542 438 EST 4.43 down 0.00601
 rc_AA215585_s_at AA215585 442 nudix (nucleoside diphosphate linked moiety X)- 3 down 0.03027
 AA215919_at AA215919 443 F-box protein 7 6.62 down 0.00921
 rc_AA218727_at AA218727 445 EST 3.47 down 0.00125
 rc_AA219039_at AA219039 446 EST 5.76 down 0.00053
 rc_AA219304_s_at AA219304 447 alpha-2-macroglobulin 21.97 down 0.00011
 rc_AA219656_at AA219653 448 EST 4.08 down 0.00607
 rc_AA223335_s_at AA223335 449 propionyl Coenzyme A carboxylase, beta 5.49 down 0.2761
 rc_AA223902_at AA22392 450 EST 9.91 down 0.00003
 rc_AA227452_at AA227452 445 EST 4.7 down 0.02345
 rc_AA227480_s_at AA22748 456 pim-2 oncogene 3.31 down 0.02413
 rc_AA227901_at AA227901 459 SEC24 (S. cerevisiae) related gene family, 3.18 down 0.00397
 rc_AA228119_at AA228119 462 pre-B-ceol colony-enhancing factor 4.77 down 0.00031
 rc_AA232114_s_at AA232114 463 epoxide hydrolase 2, cytoplasmic 24.34 down 0.00007
 rc_AA233152_at AA233152 467 EST 12.95 down 0
 rc_AA233347_at AA233347 470 zinc finger protein 216 5.9 down 0.0041
 rc_AA233369_at AA233369 471 histidine ammonia-lyase 9.06 down 0.0008
 rc_AA233763_at AA233763 472 EST 4.61 down 0.00004
 rc_AA233837_at AA233837 474 EST 4.79 down 0.0034
 rc_AA234095_at AA234095 478 EST 8.08 down 0.00394
 rc_AA234527_s_at AA234527 483 nuclear receptor subfamily 3, group C, member 1 6.19 down 0.00864
 rc_AA234561_at AA234561 485 EST 3.88 down 0.02058
 AA234634_f_at AA234634 486 CCAAT/enhancer binding protein (C/EBP), delta 7.48 down 0.03318
 AA234817_at AA234817 490 EST 6.22 down 0.00099
 rc_AA234831_at AA234831 491 EST 3.42 down 0.00206 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_AA234916_at AA234916 492 EST 3.2 down 0.00799
 rc_AA235233_at AA235233 493 EST 6.59 down 0.00755
 rc_AA235288_at AA235288 494 PTPL1-associated RhoGAP1 3.7 down 0.00643
 rc_AA235310_at AA235310 496 EST 37.86 down 0.00091
 rc_AA235507_at AA235507 498 golgi autoantigen, golgin subfamily a, 5 3.28 down 0.00249
 rc_AA235618_f_at AA235618 499 EST 3.43 down 0.2127
 rc_AA235765_s_at AA235765 501 KIAA2014 gene product 3.59 down 0.01148
 rc_AA235811_at AA235811 502 EST 3.64 down 0.01272
 rc_AA235873_s_at AA235873 505 H factor (complement)-like 1, H factor 1 9.98 down 0.01667
 rc_AA236230_at AA236230 508 EST 5.28 down 0.01517
 rc_AA236365_s_at AA236365 509 3-phosphoglycerate dehydrogenase 10.23 down 0.00562
 rc_AA236401_at AA236401 510 EST 16.71 down 0.00088
 rc_AA236455_r_at AA236455 512 EST 15.71 down 0.00286
 rc_AA236455_s_at AA236455 512 EST 11.35 down 0.02859
 rc_AA236796_s_at AA236796 517 follistatin 8.74 down 0.00862
 rc_AA236942_at AA236942 519 EST 3.18 down 0
 rc_AA236982_at AA236982 520 sterol carrier protein 2 5.56 down 0.01542
 rc_AA242766_at AA242766 523 EST 3.58 down 0.0151
 rc_AA243495_at AA243495 528 lectin, mannose-binding, 1 4.23 down 0.00179
 rc_AA243582_at AA243582 529 hemoglobin, gamma A 7.15 down 0.0021
 rc_AA243595_s_at AA243595 530 EST 3.11 down 0.008
 AA247453_at AA247453 533 EST 3.09 down 0.0015
 rc_AA250744_at AA250744 536 EST 3.36 down 0.01137
 rc_AA250775_at AA250775 537 EST 4.52 down 0.01752
 rc_AA251114_at AA251114 539 prostate cancer overexpressed gene 1 6.6 down 0.00039
 rc_AA251837_at AA251837 547 EST 3.87 down 0.00782
 quinolinate phosphoribosyltransferase (nicotinate-
 rc_AA252289_at AA252289 552 nucleotide pyrophosphorylase (carboxylating)) 5.66 down 0.01389
 rc_AA252365_at AA252365 554 EST 3.9 down 0.01796
 rc_AA253043_at AA253043 559 DKFZP586I1419 protein 3.89 down 0.00145
 AA253129_at AA253129 560 F-box protein FBL11 6.47 down 0.00001 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_AA253216_at AA253216 561 EST 28.18 down 0.00141
 rc_AA253369_s_at AA253369 563 EST 15.59 down 0.00091
 rc_AA253455_s_at AA253455 565 EST 3.05 down 0.00533
 rc_AA253459_at AA253459 566 EST 4.51 down 0.00419
 rc_AA255546_at

AA25546 569 EST 4 down 0.00301
 rc_AA255624_at AA255624 571 EST 4.06 down 0.00069
 rc_AA255878_at AA255878 572 KIAA0767 protein 3.96 down 0.00592
 rc_AA255903_at AA255903 573 CD39-like 4 5.67 down 0.01687
 rc_AA256171_at AA256171 575 EST 7.34 down 0.04562
 rc_AA256341_at AA256341 578 EST 7.37 down 0.00091
 rc_AA256367_s_at AA256367 579 paraoxonase 3 70.33 down 0.00192
 rc_AA256666_at AA256666 583 EST 4.63 down 0.0018
 rc_AA257057_s_at AA257057 586 EST 8.11 down 0.00379
 rc_AA258308_at AA258308 590 EST 5.4 down 0.00023
 rc_AA258323_at AA258323 591 EST 4.31 down 0.00046
 rc_AA258350_at AA258350 592 EST 5.08 down 0.00035
 rc_AA258353_at AA258353 593 EST 5.28 down 0.00193
 rc_AA258567_at AA258567 597 EST 6.92 down 0.00096
 rc_AA258613_at AA258613 598 EST 4.31 down 0.0344
 rc_AA258813_at AA258813 600 EST 4.63 down 0.02395
 rc_AA259064_at AA259064 602 EST 13.15 down 0.00001
 rc_AA261954_at AA261954 604 EST 7.69 down 0.00334
 rc_AA262033_s_at AA262033 606 EST 4.41 down 0.00054
 rc_AA262349_at AA262349 607 EST 3.78 down 0.00043
 rc_AA262766_at AA262766 609 EST 5.66 down 0.3832
 rc_AA279112_at AA279112 622 EST 3.42 down 0.01444
 rc_AA279533_at AA279533 627 EST 5.01 down 0.04448
 AA279550_at AA279550 628 Kruppel-like factor 4.06 down 0.00957
 rc_AA279676_s_at AA279676 630 deoxyribonuclease I-like 3 23.35 down 0.00001
 rc_AA279802_at AA279802 631 EST 3.65 down 0.03366
 rc_AA279937_at AA279937 634 EST 3.38 down 0.02719 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_AA280130_at AA280130 636 EST 4.12 down 0.00114
 spleen focus forming virus (SFFV) proviral
 rc_AA280413_s_at AA280413 638 integration oncogene spi1 4.46 down 0.02063
 rc_AA280791_at AA280791 640 eukaryotic translation initiation factor 5 3.11 down 0.03339
 rc_AA281440_at AA281440 644 EST 6.43 down 0.01246
 rc_AA281545_at AA281545 645 EST 3.64 down 0.00002
 rc_AA281591_at AA281591 646 EST 3.23 down 0.00895
 AA281677_at AA281677 648 DKFZP564M2423 protein 3.95 down 0.03606
 rc_AA281770_at AA281770 L649 seven in absentia (Drosophila) homolog 1 3.96 down 0.00094
 rc_AA281796_at AA281796 650 mannose-P-dolichol utilization defect 1 3.3 down 0.04108
 core-binding factor, runt domain, alpha subunit 2down?
 rc_AA281930_at AA281930 651 translocated to, 3 3.27 down 0.02329
 rc_AA282061_at AA282061 652 KIAA0962 protein 8.95 down 0.01033
 rc_AA282089_at AA282089 653 EST 4.93 down 0.00108
 rc_AA282179_at AA282179 655 EST 3.09 down 0.01693
 rc_AA282238_at AA282238 656 EST 3.47 down 0.00677
 rc_AA282516_at AA282516 660 7-dehydrocholesterol reductase 7.67 down 0.0008
 rc_AA282886_at AA282886 663 EST 3.57 down 0.00049
 rc_AA282971_at AA282971 665 EST 4.37 down 0.03822
 rc_AA283758_at AA283758 670 EST 3.67 down 0.04293
 AA284558_at AA284558 674 Nck, Ash and phospholipase C binding protein 3.09 down 0.00027
 rc_aa284721_s_at AA284721 677 EST 3.34 down 0.03296
 rc_AA284795_at AA284795 678 phosphatidylethanolamine N-methyltransferase 10.03 down 0.00019
 rc_AA285053_at AA285053 681 ST 6, 95 down 0.00125
 rc_AA287122_at AA287122 686 EST 3.66 down 0.00161
 rc_AA287550_f_at AA287550 689 DKFZP434C171 protein 3.53 down 0.00217
 rc_AA28756_at AW287566 690 KIAA0187 gene product 9.07 down 0.00013
 rc_AA291323_at AA291323 699 BCL2-interacting killer (apoptosis-inducing) 9.15 down 0.00514
 rc_AA291749_s_at AA291749 703 estrogen receptor 1 4.78 down 0.00059
 rc_aa292086_s_at AA292086 705 EST 5 down 0.00161
 AA292158_s_at AA292158 706 EST 21.79 down 0.00031 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_AA292328_at AA292328 707 activating transcription factor 5 17.51 down 0.00689
 rc_AA292711_at AA292711 711 EST 3 down 0.01053
 rc_AA292773_s_at AA292773 713 collagen, type XVIII, alpha 1 7.44 down 0.00158
 rc_AA293327_at AA293327 716 isocitrate dehydrogenase 1 (NADP+), soluble 7.04 down 0.04377
 rc_AA293485_at AA293485 718 EST 3.36 down 0.02799
 AA298180_at AA298180 726 EST 3.11 down 0.00747
 rc_AA299632_at

AA299632 728 EST 4.23 down 0.00371
 rc_AA312946_s_at AA312946 731 EST 9.21 down 0.00106
 AA314457_at AA314457 733 synaptonemal complex protein 3 4.86 down 0.0013
 rc_AA338512_at AA338512 742 EST 3.05 down 0.03427
 rc_AA342301_at AA342301 746 EST 3.89 down 0.00038
 rc_AA342337_at AA342337 747 EST 3.87 down 0.0069
 rc_AA342446_s_at AA342446 748 insulin receptor 6.83 down 0.00412
 rc_AA342771_at AA342771 749 EST 5.33 down 0.00331
 rc_AA343142_at AA343142 751 EST 20.87 down 0.00003
 rc_AA344866_s_at AA344866 752 complement component 8, gamma polypeptide 7.28 down 0.00206
 rc_AA347674_at AA347674 753 EST 10.59 down 0.03716
 rc_AA347717_at AA347717 754 EST 5.25 down 0.00207
 rc_AA348284_at AA348284 755 EST 4.54 down 0.00759
 rc_AA348466_s_at AA348466 756 regulator of G-protein signalling 5 3.2 down 0.00571
 rc_AA348485_at AA348485 757 KIAA0438 gene product 4.01 down 0.04563
 fatty-acid-Coenzyme A ligase, long-chain 1, fatty-
 rc_AA348922_s_at AA348922 758 acid-Coenzyme A ligase, long-chain 2 64.27 down 0.0002
 rc_AA349836_at AA349836 760 EST 3.01 down 0.00911
 KIAA0382 protein down? leukemia-associated rho
 rc_AA370359_s_at AA370359 767 guanine nucleotide exchange factor 9GEF) 4.82 down 0.01077
 AA376875_at AA376875 770 monoamine oxidase A 3.8 down 0.02746
 rc_AA377087_at AA377087 771 EST 16.75 down 0.0002
 rc_AA381125_at AA381125 772 EST 15.48 down 0
 rc_AA382975_f_at AA382975 773 EST 3.7 down 0.00131
 rc_AA393825_at AA393825 776 EST 3.62 down 0.0065 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 AA393961_at AA393961 777 EST 3.7 down 0.01029
 AA397841_at AA397841 780 EST 8.21 down 0
 rc_AA397914_at AA397914 783 EST 3.16 down 0.0033
 rc_AA398102_at AA398102 786 KIAA0429 gene product 6.22 down 0.00396
 rc_AA398124_s_at AA398124 787 growth factor receptor-bound protein 14 7.82 down 0.00009
 rc_AA398221_at AA398221 790 calcium/calmodulin-dependent protein kinase 3.78 down .00019
 rc_AA398257_at AA398257 791 7-dehydrocholesterol reductase 4.43 down 0.04169
 rc_AA398280_at AA398280 792 EST 12.43 down 0.00134
 rc_AA398386_at AA398386 793 EST 5.71 down 0.00007
 rc_AA398422_i_at AA398422 794 EST 3.94 down 0.00388
 rc_AA398423_at AA398423 795 EST 8.26 down 0.00063
 rc_AA398445_at AA398445 796 EST 4.28 down 0.01764
 rc_AA398892_at AA398892 800 similar to yeast BET3 (S. cerevisiae) 7.43 down 0.00038
 rc_AA40030_at AA40030 806 EST 3.98 down 0.00088
 rc_AA400246_at AA400246 810 mitogen-activated protein kinase-activated 3.09 down 0.00476
 rc_AA400251_at AA400251 811 EST 4.07 down 0.00032
 rc_AA400258_at AA400258 812 EST 11.89 down 0.00478
 rc_AA400259_at AA400259 813 EST 3.65 down 0.00476
 rc_AA400471_at AA400471 816 EST 5.45 down 0.0056
 rc_AA400780_at AA400780 818 EST 3.5 down 0.00107
 rc_AA400831_at AA400831 819 EST 3.49 down 0.00105
 rc_AA400834_f_at AA400834 820 EST 4.73 down 0.01523
 rc_AA400864_at AA400864 821 down 7.51 down 0.02237
 rc_AA400915_at AA400915 823 EST 9.84 down 0.00351
 rc_AA400934_at AA400934 824 EST 4.98 down 0.02013
 rc_AA400979_at AA400979 825 calcitonin receptor-like receptor activity modifying 6.65 down 0.01051
 rc_AA401151_at AA401151 827 lysozyme (renal amyloidosis) 3.01 down 0.0051
 rc_AA401343_at AA401343 828 EST 3.11 down 0.01929
 rc_AA401376_at AA401376 829 EST 3.97 down 0.00797
 rc_AA401562_s_at AA401562 830 EST 50.45 down 0.00301
 AA402006_at AA402006 834 EST 4.19 down 0.00094 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 AA402095_s_at AA402095 835 EST 3.12 down 0.01412
 rc_AA402224_at AA402224 836 growth arrest and DNA-damage-inducible, 14.41 down 0.0012
 rc_AA402656_at AA402656 841 EST 12.05 down 0.00001
 rc_AA402799_at AA402799 842 EST 11.81 down 0.00031
 AA404252_at AA404252 848 lectin, mannose-binding, 1 16.15 down 0.0001
 rc_AA404352_at AA404352 850 EST 7 down 0.00059
 rc_AA404500_at AA404500 852 EST 4.16 down 0.01375
 rc_AA405819_at AA405819 865 KIAA0668 protein 8.59 down 0.02034
 rc_AA405832_at AA405832 866 EST 12.24 down 0.00441
 rc_AA405907_at

AA405907 867 EST 3.12 down 0
 rc_aa406125_s_at AA406125 868 EST 4.95 down
 0.01027
 rc_AA406126_at AA406126 869 EST 8.43 down 0.00569
 rc_AA406231_s_at
 AA406231 873 KIAA0381 protein 4.46 down 0.04049
 AA406435_s_at AA406435 877 EST 3.24
 down 0.00941
 rc_AA410181_at AA410181 881 EST 3 down 0.00268
 rc_AA410255_at
 AA410255 882_s_at 7.56 down 0.00043
 rc_AA410507_at AA410507 884 EST 3.73 down
 0.01703
 rc_AA410523_at AA410523 886 EST 6.37 down 0.03506
 rc_AA411764_at
 AA411764 891 similar to APOBEC1 4 down 0.01491
 rc_AA412034_at AA412034 894 EST 3.09
 down 0.02309
 rc_AA412063_at AA412063 895 EST 8.26 down 0.0001
 rc_AA412184_at
 AA412184 898 EST 3.08 down 0.00012
 rc_AA412481_s_at AA412481 902 EST 8.07 down
 0.00014
 rc_AA416723_at AA416723 906 EST 3.57 down 0.01042
 rc_AA416740_s_at
 AA416740 907 EST 3.08 down 0.01592
 rc_AAE16873_at AA416873 908 EST 7.82 down
 0.00005
 sphingomyelin phosphodiesterase 1, acid
 rc_AA416890_s_at AA416890 909
 lysosomal (acid sphingomyelinase) 6.6 down 0.00112
 5-methyltetrahydrofolate-
 homocysteine
 rc_AA416936_at AA416936 910 methyltransferase reductase 4.98 down
 0.00632
 rc_AA417046_at AA417046 915 fatty-acid-Coenzyme A ligase, very long-chain 1 44
 down 0 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID
 Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_AA417078_at AA417078
 916 EST 4.1 down 0.00414
 rc_AA417373_at AA417373 917 EST 4.8 down 0.01342

 rc_AA417375_at AA417375 918 EST 4.21 down 0.00231
 AA418098_at AA418098 920 cAMP
 responsive element binding protein-like 2 3.18 down 0.03824
 cytochrome P450, subfamily I
 (aromatic
 rc_AA418907_s_at AA418907 922 compound-inducible), polypeptide 1 4.05 down
 0.04276
 AA419507_at AA419507 924 EST 5.58 down 0.00578
 rc_AA419608_at AA419608
 925 EST 9.19 down 0.00005
 rc_AA419622_at AA419622 926 EST 4.62 down 0.00386

 rc_AA421049_at AA421049 927 activating transcription factor 5 44.41 down 0.00179

 rc_AA421052_at AA421052 929 branched chain alpha-ketoacid dehydrogenase 3.52
 down 0.00869
 rc_AA421244_s_at AA421244 932 SH3-domain binding protein 5 (BTK-
 associated) 4.32 down 0.007
 rc_AA421561_at AA421561 933 insulin-like growth factor 2
 (somatomedin A) 9.98 down 0.00007
 AA424307_at AA424307 944 EST 5.73 down 0.0074

 rc_AA424672_s_at AA424672 946 dermatopontin 4.69 down 0.00843
 rc_AA424798_at
 AA424798 947 EST 17.45 down 0.00352
 rc_AA424813_at AA424813 948 EST 5.77 down
 0.00503
 rc_AA425294_at AA425294 952 EST 10.61 down 0.00083
 rc_AA425309_at
 AA425309 953 nuclear factor I/B 4.9 down 0.00466
 rc_AA425782_at AA425782 956 KIAA0874
 protein 5.52 down 0.03433
 rc_AA425836_at AA425836 957 EST 4.55 down 0.00035

 AA426156_at AA426156 959 EST 3.67 down 0.00153
 AA426168_at AA426168 960 KIAA0805
 protein 3.73 down 0.01477
 AA426304_s_at AA426304 962 EST 6.61 down 0.01092

 rc_AA426330_at AA426330 963 N-acylsphingosine amidohydrolase (acid 4.24 down 0.00668

 rc_AA426468_at AA426468 966 EST 3.38 down 0.0099
 rc_AA426609_at AA426609 968 EST
 6.28 down 0.01233
 rc_AA427778_at AA427778 978 EST 3.57 down 0.00368

 rc_AA427783_at AA427783 979 EST 4.37 down 0.0004
 rc_AA427819_at AA427819 980 midline
 2 3.44 down 0.00063
 AA428006_at AA428006 984 DKFZP564B167 protein 3.71 down 0.02325
 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank
 Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_AA428150_at AA428150 985 EST
 5.24 down 0.00167
 rc_AA427325_at AA428325 988 EST 8.36 down 0.00002

 rc_AA428567_at AA428567 989 EST 3.99 down 0.00788
 rc_AA428607_at AA428607 990
 ribosomal protein S5 pseudogene 1 4.21 down 0.04305
 rc_AA428863_at AA428863 991 EST 3.5
 down 0.01726
 rc_AA428900_at AA428900 992 EST 7.01 down 0.00037
 rc_AA429038_at
 AA429038 995 EST 3.29 down 0.00927
 rc_AA429478_at AA429478 998 EST 3.41 down
 0.02599
 rc_AA429904_at AA429904 1005 EST 7.26 down 0.00524
 AA430011_at
 AA430011 1006 EST 8.35 down 0.00729
 rc_AA430026_at AA430026 1007 EST 3.31 down
 0.00786
 rc_AA430028_at AA430028 1008 EST 9.14 down 0.00246
 rc_AA430044_at
 AA430044 1010 EST 7.78 down 0.00124
 rc_AA430047_at AA430047 1011 EST 3.44 down

0.0016
 rc_AA430108_at AA430108 1013 EST 3.8 down 0.04484
 rc_AA430666_at AA430666 1016 EST 5.12 down 0.00377
 rc_AA431337_at AA431337 1020 EST 6.26 down 0.00053
 rc_AA431462_at AA431462 1022 EST 4.45 down 0.00956
 rc_AA431480_s_at AA431480 1023 EST 4.3 down 0.0086
 rc_AA431773_at AA431773 1026 EST 7.61 down 0.00063
 rc_AA432168_at AA432168 1031 S-adenosylhomocysteine hydrolase-like 1 4.71 down 0.01377
 rc_AA433946_at AA433946 1033 EST 43.74 down 0.00005
 rc_AA435591_at AA435591 1038 kinesin family member 3B 3.5 down 0.0001
 rc_AA435753_at AA435753 1045 EST 4.71 down 0.00078
 solute carrier family 25 (mitochondrial carrier;
 rc_AA435777_f_at AA435777 1047 citrate transporter), member 1 7.48 down 0.00613
 rc_AA435824_at AA435824 1048 EST 3.93 down 0.02764
 rc_AA435985_at AA435985 1049 EST 17.7 down 0
 rc_AA436489_at AA436489 1053 EST 7.34 down 0.001
 rc_AA436560_at AA436560 1055 claudin 1 11.41 down 0.00756
 rc_AA436690_at AA436690 1057 EST 4.58 down 0.00948 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_AA436880_at AA436880 1058 EST 3.22 down 0.00699
 rc_AA436926_at AA436926 1059 EST 5.5 down 0.00984
 rc_AA437235_s_at AA437235 1060 EST 7.15 down 0.01455
 rc_AA437265_s_at AA437265 1061 EST 4.39 down 0.00826
 rc_AA437295_at AA437295 1062 ribosomal protein L7a 4.35 down 0.00347
 rc_AA441791_at AA441791 1065 EST 3.58 down 0.00357
 rc_AA442334_at AA442334 1069 EST 7.15 down 0.00018
 rc_AA442342_at AA442342 1070 EST 5.62 down 0.00052
 rc_AA443272_at AA443272 1074 EST 7.68 down 0.00869
 rc_AA443658_at AA443658 1079 transmembrane 7 superfamily member 2 9.06 down 0.00048
 rc_AA443756_at AA443756 1080 EST 5.05 down 0.00341
 rc_AA443822_at AA443822 1082 EST 5.46 down 0.02538
 rc_AA443934_at AA443934 1083 GTP-binding protein Rho7 3.09 down 0.00214
 rc_AA443936_s_at AA443936 1084 EST 22.96 down 0.00627
 rc_AA443993_at AA443993 1086 EST 3.21 down 0.02948
 rc_AA446342_at AA446342 1088 seven in absentia (Drosophila) homolog 1 4.84 down 0.00015
 rc_AA446587_at AA446587 1091 EST 5.8 down 0.00012
 rc_AA446651_at AA446651 1093 EST 3.14 down 0.01902
 rc_AA446666_at AA446666 1094 EST 4.03 down 0.02369
 UDP-N-acteylglucosamine pyrophosphorylase 1;
 rc_AA447549_at AA447549 1101 Sperm associated antigen 2 6.37 down 0.02815
 rc_AA447617_at aa447617 1103 est 3.26 down 0.04687
 rc_AA447740_at AA447740 1106 EST 3.22 down 0.02518
 rc_AA447971_at AA447971 1110 EST 8.08 down 0.00035
 rc_AA447977_s_at AA447977 1111 EST 3.84 down 0.00045
 rc_AA448002_at AA448002 1113 putative type II membrane protein 10.05 down 0
 rc_AA448282_at AA448282 1115 EST 3.87 down 0.00217
 FXYD domain-containing ion transport regulator 1
 rc_AA448300_at AA448300 1115 (phospholemman) 24.97 down 0.00001
 rc_AA449267_at AA449267 1120 EST 16.44 down 0.00926
 rc_AA449297_at AA449297 1121 EST 3.78 down 0.00039 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_AA448395_at AA448395 1122 EST 5.01 down 0.0006
 rc_AA449327_at AA449327 1123 EST 4.77 down 0.01248
 rc_AA449448_at AA449448 1125 EST 3.97 down 0.00103
 rc_AA450114_at AA450114 1131 EST 4.96 down 0.01238
 rc_AA450127_at AA450127 1132 growth arrest and DNA-damage-inducible, beta 7.98 down 0.00078
 rc_AA450281_at AA450281 1134 EST 5.55 down 0.00004
 rc_AA451836_at AA451836 1137 EST 4.9 down 0.01412
 rc_AA451911_at AA451911 1139 EST 3.44 down 0.00221
 rc_AA452158_at AA452158 1141 ras homolog gene family, member B 28.96 down 0.00064
 rc_AA452454_at AA452454 1144 EST 4.45 down 0.00179
 rc_AA452549_at AA452549 1146 platelet-derived growth factor receptor, alpha 3.3 down 0.04155
 rc_AA452559_s_at AA452559 1147 EST 4.35 down 0.00804
 rc_aa452598_s_at AA452598 1148 genethonin 1 5.49 down 0.00163
 rc_AA452855_at AA452855 1150 lectin, mannose-binding, 1 9.88 down 0.00428
 rc_AA452860_at AA452860 1151 EST 3.99 down 0.00831
 rc_AA452915_at AA452915 1152 EST 3.13 down 0.00561
 rc_AA453770_s_at AA453770 1157 EST 6.04 down 0.00524
 rc_AA453917_at AA453917 1159 EST 3.3 down 0.01896

rc_AA453988_at AA453988 1160 methionine adenosyltransferase I, alpha 54.29 down 0.00381

rc_AA454086_f_at AA454086 1161 UDP-glucose dehydrogenase 4.29 down 0.00981

rc_AA454159_at AA454159 1162 EST 10.81 down 0.00132
 rc_AA454170_at AA454170 1163
EST 3.11 down 0.03
 rc_AA454177_i_at AA454177 1164 EST 10.3 down 0.0008

rc_AA454184_at AA454184 1165 EST 3.96 down 0.04605
 rc_AA454733_s_at AA454733 1169
EST 5.61 down 0.01182
 rc_AA455097_i_at AA455097 1172 EST 6.03 down 0.00419

rc_AA455367_at AA455367 1176 DKFZP586F1018 protein 3.73 down 0.00202
 AA455403_at
AA455403 1177 EST 15.46 down 0.01547
 rc_AA455865_at AA455865 1180
phosphatidylinositol glycan, class B 5.41 down 0.00004
 rc_AA455806_s_at AA455896 1181
glypican 1 3.46 down 0.00887
 rc_AA455962_at AA455962 1182 EST 3.1 down 0.03905 Table
6B. Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank Seq
ID Known Gene Name Fold Change Direction Pvalue
 rc_AA455987_at AA455987 1183 EST
5.36 down 0.00029
 butyrobetaine (gamma), 2-oxoglutarate
 rc_AA455988_at AA455988
1184 dioxygenase (gamma-butyrobetaine hydroxylase) 15.54 down 0.00001
 rc_AA456055_at
AA456055 1185 EST 5.16 down 0.00158
 rc_AA456147_at AA456147 1188 general transcription
factor IIIA 4.23 down 0.00088
 rc_AA456289_at AA456289 1189 EST 15.31 down 0.00004

rc_AA456311_s_at AA456311 1190 EST 46.81 down 0.001
 rc_AA456326_at AA456326 1191
EST 3.35 down 0.00489
 rc_AA456589_at AA456589 1194 EST 4.23 down 0.00102

AA456687_at AA456687 1197 EST 3.08 down 0.01189
 rc_AA457377_at AA457377 1201 EST
3.1 down 0.00549
 rc_AA458652_at AA458652 1202 EST 8.26 down 0.00001

rc_AA458923_at AA458923 1207 EST 3.36 down 0.00421
 rc_AA458946_at AA458946 1209
EST 15.88 down 0.00004
 rc_AA459256_at AA459256 1212 lectin, mannose-binding, 1 3.01
down 0.00094
 rc_AA459293_at AA459293 1213 EST 3.2 down 0.0001
 rc_AA459389_at
AA459389 1216 tyrosylprotein sulfotransferase 2 3.72 down 0.02252
 rc_AA459420_at
AA459420 1217 EST 7.25 down 0.0214
 rc_AA459668_at AA459668 1219 3-hydroxyisobutyryl-
Coenzyme A hydrolase 7.62 down 0.00225
 rc_aa459690_s_at AA459690 1221 EST 9.18 down
0.00732
 solute carrier family 22 (extraneuronal
 rc_AA460012_at AA460012 1224
monoamine transporter), member 3 4.27 down 0.04975
 AA460047_at AA460047 1226 EST 3.33
down 0.04011
 AA460128_at AA460128 1227 similar to S. pombe din1+ 3.28 down
0.01299
 rc_AA460449_at AA460449 1228 EST 7.77 down 0.00011
 rc_AA460661_at
AA460661 1229 EST 7.02 down 0.00053
 rc_AA460916_at AA460916 1233 EST 3.69 down
0.04841
 rc_AA461057_at AA461057 1234 nuclear localization signal deleted in 5.22 down
0.00051
 rc_AA461303_at AA461303 1238 DKFZP586D 1519 protein 4.77 down 0.0438

rc_AA461444_at AA461444 1239 EST 11.58 down 0.00167
 rc_AA461458_at AA461458 1241
EST 3.37 down 0.02427 Table 6B. Down regulated in metastatic cancers versus normal sample set
2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue

rc_AA463194_s_at AA463194 1244 KIAA1037 protein 4.92 down 0.01866
 rc_AA463195_at
AA463195 1245 EST 3.41 down 0.00413
 AA463311_at AA463311 1248 EST 3.71 down
0.04902
 rc_AA463729_at AA463729 1250 EST 4.07 down 0.00676
 rc_AA463876_at
AA463876 1252 EST 3.31 down 0.00109
 rc_AA463946_at AA463946 1254 pigment epithelium-
derived factor 3.38 down 0.0018
 rc_AA464188_s_at AA464188 1256 EST 4.82 down
0.03208
 rc_AA464603_at AA464603 1260 EST 3.26 down 0.0007
 rc_AA465240_at
AA465240 1270 EST 4.03 down 0.0046
 rc_AA470153_at AA470153 1275 solute carrier family
21 (organic anion 13.26 down 0.00315
 rc_AA476324_s_at AA476324 1281 EST 55.22 down
0.00132
 rc_AA476346_at AA476346 1283 EST 3.12 down 0.01067
 rc_AA476352_at
AA476352 1284 EST 3.41 down 0.02233
 rc_AA477119_at AA477119 1289 EST 3.13 down
0.0338
 AA477919_at AA477919 1293 EST 4.69 down 0.00141
 AA477978_s_at
AA477978 1294 short-chain dehydrogenase/reductase 1 8.53 down 0.01651
 rc_AA478416_at
AA478416 1300 EST 4.04 down 0.00078
 rc_AA478441_at AA478441 1302 cathepsin F 5.07
down 0.00752
 AA479132_at AA479132 1309 EST 3.12 down 0.00876
 rc_AA479148_at
AA479148 1311 EST 38.05 down 0
 rc_AA479488_at AA479488 1313 S-adenosylhomocysteine

hydrolase-like 1 4 down 0.0269
 rc_AA479498_at AA479498 1314 EST 5.78 down 0.01489
 rc_AA479885_at AA479885 1318 KIAA0843 protein 15.57 down 0.00024
 rc_AA479968_s_at AA479968 1321 arylsulfatase A 9.01 down 0.00224
 rc_AA480975_at AA480975 1322 EST 8.95 down 0.00259
 rc_AA480991_s_at AA480991 1323 EST 8.59 down 0.00156
 rc_AA481432_s_at AA481432 1328 fibronectin 1 7.76 down 0.0061
 rc_AA481526_at AA481526 1329 EST 3.73 down 0.00002
 AA481670_at AA481670 1330 retinal short-chain dehydrogenase/reductase 6.2 down 0.0078
 rc_AA482594_at AA482594 1337 EST 5.42 down 0.00387
 rc_AA485089_at AA485089 1341 EST 5.46 down 0.00044 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_AA485326_at AA485326 1342 ATP-binding cassette, sub-family D (ALD), 3.08 down 0.00415
 rc_AA485413_at AA485413 1344 EST 4.54 down 0.00137
 aldehyde dehydrogenase 5 family, member A1
 rc_AA486410_at AA486410 1348 (succinate-semialdehyde dehydrogenase) 8.08 down 0.00485
 AA486511_at AA486511 1349 EST 22.21 down 0.00113
 rc_AA486567_at AA486567 1350 EST 5 down 0.00002
 rc_AA487161_at AA487161 1353 ubiquilin 2 3.13 down 0.0023
 rc_AA487603_at AA487503 1356 EST 8.85 down 0.00012
 rc_AA487606_at AA487606 1358 EST 3.05 down 0.00291
 rc_AA488843_at AA488843 1362 comichon-like 8.58 down 0.02131
 rc_AA489061_at AA489061 1367 EST 3.49 down 0.00223
 rc_AA489629_at AA489629 1369 EST 8.08 down 0.00109
 rc_AA489636_at AA489636 1370 EST 10.7 down 0
 rc_AA489798_at AA489798 1373 hypothetical protein, estradiol-induced 875 down 0.00544
 rc_AA490159_at AA490159 1374 glucose-6-phosphatase, transport (glucose-6- 5.44 down 0
 rc_AA490214_at AA490214 1376 EST 3.12 down 0.02382
 rc_AA490620_at AA490620 1378 EST 4.77 down 0.00201
 rc_AA490670_at AA490670 1379 EST 9.96 down 0.00454
 UDP-N-acetylglucosamine-2-epimerase/N-
 AA490775_AT AA490775 1380 acetylmannosamine kinase 5.34 down 0.0018
 rc_AA490882_s_at AA490882 1381 EST 3.29 down 0.00319
 rc_AA490890_AT aa490890 1382 EST 3.02 down 0.00007
 rc_AA491000_AT aa491000 1385 EST 4.23 down 0.02305
 rc_AA491001_i_at AA491001 1386 EST 8.52 down 0.01118
 rc_AA491001_f_at AA491001 1386 EST 3.73 down 0.01957
 AA495758_s_at AA495758 1391 EST 3.94 down 0.00772
 rc_AA495820_at AA495820 1393 EST 3.98 down 0.00218
 rc_AA496053_at AA496053 1396 EST 3.28 down 0.00095
 AA496423_at AA496423 1399 WW domain binding protein 2 3.52 down 0.01314
 rc_AA496914_at AA496914 1401 v-maf musculoaponeurotic fibrosarcoma (avian) 3.48 down 0.00361
 rc_AA497052_at AA497052 1408 DKFZP727G051 protein 7.28 down 0.01745 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_AA504492_at AA504492 1414 tubulin, alpha, ubiquitous 4.21 down 0.00752
 AA50-5198_at AA505198 1419 EST 3.41 down 0.0343
 rc_AA521920_at AA521290 1421 EST 4.53 down 0.0148
 rc_AA521292_at AA521292 1422 EST 8.58 down 0.00064
 rc_AA521306_at AA521306 1423 EST 4.27 down 0.00567
 UDP-N-acetylglucosamine-2-epimerase/N-
 rc_AA598417_AT AA598417 1426 acetylmannosamine kinase 8.56 down 0.01638
 rc_AA598419_s_at AA598419 1427 translational inhibitor protein p14.5 23.6 down 0.00036
 rc_AA598675_at AA598675 1433 EST 3.25 down 0.03934
 rc_AA598679_at AA598679 1434 EST 5.37 down 0.00467
 rc_AA598746_at AA598746 1437 EST 3.8 down 0.02667
 rc_AA598926_at AA598926 1441 EST 3.7 down 0.00432
 rc_AA599211_at AA599211 1445 short-chain dehydrogenase/reductase 1 7.85 down 0.00911
 rc_AA599234_s_at AA599234 1447 murine leukemia viral (bmi-1) oncogene homology 3.9 down 0.0068
 rc_AA599472_at AA599472 1451 succinate-CoA ligase, GDP-forming, beta subunit 5.07 down 0.00447
 rc_AA599526_at AA599526 1453 cartilage associated protein 3.02 down 0.00043
 rc_AA599814_at AA599814 1456 EST 12.37 down 0.00002
 rc_AA599937_s_at AA599937 1458 insulin-like growth factor-binding protein 4 26.92 down 0.00094
 rc_AA599954_at AA599954 1459 cell cycle progression 8 protein 3.15 down 0.00021
 rc_AA608546_at AA608546 1463 EST 12.52 down 0.00003
 rc_AA608671_at AA608671 1466 EST 3.14 down 0.04543
 rc_AA608729_at AA608729 1468

EST 3.89 down 0.01757
 rc_AA608751_i_at AA608751 1469 EST 5.76 down 0.01404
 rc_AA608802_at AA608802 1470 EST 6.95 down 0.00263
 rc_AA608807_s_at AA608807 1471 inhibin, beta B (activin AB beta polypeptide) 4.05 down 0.005688
 rc_AA608837_at AA608837 1472 EST 6.2 down 0.00006
 rc_AA609011_at AA609011 1476 EST 3.94 down 0.0313
 rc_AA609164_at AA609164 1480 cytochrome b-561 6.8 down 0.02298
 rc_AA609316_at AA609316 1481 EGF-like-domain, multiple 5 7.97 down 0.00011
 rc_AA609519_at AA609519 1482 EST 8.13 down 0.00009
 rc_AA609537_s_at AA609537 1483 hepatic leukemia factor 8.76 down 0.00018 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_AA609572_at AA609572 1484 EST 3.02 down 0.01534
 rc_AA609574_at AA609574 1485 EST 5.03 down 0
 rc_AA609576_at AA609576 1486 EST 3.1 down 0.00266
 rc_AA609773_at AA609773 1489 EST 6.09 down 0.01103
 rc_AA609774_at AA609774 1490 EST 4.02 down 0.00424
 rc_AA609934_at AA609934 1493 EST 6.84 down 0.00048
 rc_AA609996_at AA609996 1495 EST 3.93 down 0.00988
 rc_AA620343_at AA620343 1500 EST 5.04 down 0.00407
 rc_AA620556_at AA620556 1505 EST 32.4 down 0.00353
 rc_AA620667_s_at AA620667 1506 protein tyrosine phosphatase type IVA, member 1 5.92 down 0.00206
 rc_AA620830_at AA620830 1509 DKFZP564I122 protein 3.42 down 0.02421
 rc_AA621131_at AA621131 1513 EST 35.37 down 0
 rc_AA621192_at AA621192 1515 EST 5.39 down 0.0016
 rc_AA621209_at AA621209 1516 similar to Caenorhabditis elegans protein 6.34 down 0.00144
 rc_AA621235_at AA621235 1517 EST 3.44 down 0.0021
 rc_AA621274_i_at AA621274 1519 EST 7.43 down 0.00065
 rc_AA621430_at AA621430 1525 doublecortin; lissencephaly, X-linked 3.09 down 0.00024
 rc_AA621796_at AA621796 1531 kinesin family member 3B 4.44 down 0.00032
 PDZ domain containing guanine nucleotide
 AB002311_at AB002311 1535 exchange factor (GEF) 1; RA(Ras/Rap1A- 4.21 down 0.00476
 AB002328_at AB002328 1536 calcineurin binding protein 1 5.55 down 0.00016
 AF000573_ma1-at AF000573 143 homogentisate 1,2-dioxygenase (homogentisate 13.76 down 0.00002
 AF005039_at AF005039 1548 secretory carrier membrane protein 3 3.42 down 0.04953
 solute carrier family 4, sodium bicarbonate
 AF007216_at AF007216 1550 cotransporter, member 4 5.79 down 0.00005
 C01257_at C01257 1554 EST 5.35 down 0.00608
 C01286_s_at C01286 1555 integral membrane protein 2B 4.11 down 0.00292
 C01409_s_at C01409 1556 EST 4.41 down 0.01725
 C01686_at C01686 1557 EST 3.01 down 0.00048
 C02099_s_at C02099 1560 CGI-131 protein 5.85 down 0.02377
 C02460_at c02460 1562 EST 3.64 down 0.02705 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_C14963_s_at C14963 1572 nicotinamide nucleotide transhydrogenase 3.9 down 0.0044
 C15871_at C15871 1575 EST 3.26 down 0.00046
 C16420_s_at C16420 1576 EST 5.95 down 0.00119
 rc_C20653_at C20653 1578 EST 10.59 down 0.00001
 rc_C20810-at C20810 1579 EST 5.17 down 0.00614
 rc_C20911_at C20911 1580 antithrombin III 6.56 down 0.00175
 rc_C20974_at C20974 1581 Vanin 1 6.66 down 0.00272
 rc_C21130_at C21130 1583 EST 8.79 down 0.00008
 rc_C21238_at C21238 1584 EST 4.54 down 0.02074
 cytochrome P450, subfamily IIIA (niphedipine
 D00003_s_at D00003 1586 oxidase), polypeptide 3 22.05 down 0.00059
 cytochrome P450, subfamily IIIa (niphedipine
 D00003_at D00003 1586 oxidase), polypeptide 3 9.46 down 0.00001
 D00097_s_at D00097 1588 amyloid P component, serum 16.72 down 0.0098
 cytochrome P450, subfamily IIIA (niphedipine
 oxidase), polypeptide 3, cytochrome p450,
 subfamily IIIA (niphedipine oxidase), polypeptide
 D00408_s_at D00408 1589 5, cytochrome P450, subfamily IIIA, polypeptide 7 11.1 dwn 0
 D00632_at D00632 1591 glutathione peroxidase 3 (plasma) 6.55 down 0.00121
 D00723_at D00723 1592 glycine cleavage system protein H (aminomethyl 4.18 down 0.00543
 D10040_at D10040 1593 fatty-acid-Coenzyme A ligase, long-chain 2 20.51 down 0
 acetyl-coenzyme A cactyltransferase 1
 D10511_at D10511 1594 (acetoacetyl Coenzyme A thiolase) 10.68 down 0.0002
 rc_D11756)_f_at D11756 1596 EST 5.49 down 0.01272
 rc_D11802_at D11802 1597 angiotensinogen 5.65 down

0.00009
 rc_D11835_at D11835 1598 low density lipoprotein receptor (familial 21.76 down
0.00307
 rc_D1881_at D11881 1599 KIAA0962 protein 4.37 down 0.01627

phosphodiesterase 1/nucleotide pyrophosphatase
 D12485_at D12485 1600 1 (homologous to ouse
LY-41 antigen) 4.57 down 0.00008 Table 6B. Down regulated in metastatic cancers versus normal
sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction
Pvalue
 cytochrome P450, subfamily IVF, polypeptide
 2, cytochrome p450, subfamily IVF,
polypeptide 3
 D12620-s_at D1262 1601 (leukotriene B4 omega hydroxylase) 35.09 down
0.00015
 cytochrom P450, subfamily IVF, polypeptide
 2, cytochrome P450, subfamily IVF
polypeptide 3
 D12620_s_at D12620 1601 (leukotriene B4 omega hydroxylase) 13.45 down
0
 D13243_s_at D13243 1602 pyruvate kinase, liver and RBC 20.22 down 0
 D13643_at
D13643 1609 KIAA0018 gene product 10./84 down 0.00058
 D13705_s_at D13705 1610
cytochrome P450, subfamily IVAm, polypeptide 11 3.7 down 0.00038
 D13814_s_at D13814
1611 angiotensin receptor 1, angiotensin receptor 1B 3.12 down 0.00101
 D14012_s_at D14012
1612 HGF activator 12.75 down 0.0035
 D14664_at D14664 1616 KIAA0022 gene product 8.98
down 0.00011
 D14695_at D14695 1618 KIAA025 gene product: MMS-inducible gene 6.48 down
0
 acetyl-Coenzyme A acyltransferase 2
 D16294_at D16294 1619 (mitochondrial 3-oxoacyl-
Coenzyme A thiolase) 4.81 down 0.03921
 D16350_at D16350 1620 SA (rat hypertension-
associated) homology 383 down 0.00117
 hydroxyacyl-Coenzyme A dehydrogenase/3-

ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme
 D16481_at D16481 1621 A hydratase
(trifunctional protein), beta subunit 3.18 down 0.00695
 D16626_at D16626 1622 histidine
ammonia-lyase 22.66 down 0
 D16626_at D16626 1622 histidine ammonia-lyase 925 down
0.00025
 rc_D20350_at D20350 1624 EST 13.97 down 0.00057
 D31117_at D31117 1640
ribosome binding protein 1 (dog 180kD homolog)_ 5.3 down 0.02749
 D31225_at D31225 1641
EST 3.17 down 0.01073
 D31289_at D31289 1642 EST 4.16 down 0.02166
 D31381_at
D31381 1644 dynei, axonemal, light polypeptide 4 4.97 down 0.01806
 D31628_s_at D31628
1646 4-hydroxyphenylpyruvate dioxygenase 50.48 down 0.00002
 D31716_at D31716 1647 basic
transcription element binding protein 1 5.35 down 0.00086
 D31815_at D31815 1648 regucalcin
(senescence marker protein-30) 10.55 down 0.00037
 d31887_at D31887 1649 KIAA0062 protein
4.26 down 0.00101
 D37931_at D37931 1650 ribonuclease, RNase A family, 4 5.81 down 0.00836
Table 6B. Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank
Seq ID Known Gene Name Fold Change Direction Pvalue
 inter-alpha (globulin)_ inhibitor H4
(plasma
 D38535_at D38535 1654 Kallikrein-sensitive glycoprotein) 13.2 down 0.01165

rc_D45529_at D45529 1662 EST 3.82 down 0.00193
 rc_D45556_at D45556 1663 EST 4.83
down 0.01044
 rc-D45714_at D45714 1664 EST 5.64 down 0.00384
 D49357_at D49357
1665 methionine adenosyltransferase I, alpha 11.28 down 0.00331
 D49387-at D49387 1666
NADP dependent leukotriene b4 12- 8.17 down 0.00972
 D49742_at D49742 1668 hyaluronan-
binding protein 2 18.13 down 0.00012
 rc_D51199_at D51199 1677 EST 5.05 down 0.00192

rc_D51279_s-at D51279 1679 ovarian granulosa cell protein (13kD) 5.88 down 0.01271

rc_D52097_s_at D52097 1682 prostatic binding protein 8.1 down 0.00141
 D57823_at D57823
1690 Sec23 (S. cerevisiae) homolog A 4.43 down 0
 D58231_s_at D58231 1692 ubiquitin-like 3
3.07 down 0.0002
 rc_D59344_s_at D59344 1695 EST 3.34 down 0.01337
 rc_D59554_f-at
D59544 1698 EST 6.7 down 0
 rc_D59714_s_at D59714 1700 mitogen inducible 2 17.62 down
0.00014
 rc_D60670_at D60670 1702 EST 3.73 down 0.00382
 rc_D60769_s_at D60769
1703 KIAA0096 protein 4.31 down 0.00142
 rc_D60856_f_at D60856 1705 UDP-glucose
dehydrogenase 6.45 down 0.01222
 D61991_at D61991 1706 EST 4.84 down 0.00005

D62103_s_at D62103 1707 EST 4.11 down 0.0263
 rc_D62518_at D62518 1708 EST 17.49 down
0.00017
 D63160_at D63160 1709 ficolin (collagen/fibrinogen domain-containing 4.01 down
0.00391
 D78011_at D78011 1717 dihydropyrimidinase 21.37 down 0.00003
 D79276 at
D79276 1722 succinate-CoA ligase, GDP-forming, beta subunit 6.8 down 0.00047
 D79687_at
D79687 1723 KIAA1053 protein 5.06 down 0.00047
 rc_D80050_at D80050 1726 EST 4.64 down
0.01001
 rc_D80217_f-at D80217 1727 H91620p protein 3.61 down 0.01973
 rc_D80218-

f_at D80218 1728 brain acid-souble protein 1 3.83 down 0.0137
 rc_D80312_f_at D80312 1730 EST 3.74 down 0.01909
 rc_D80408_at D80408 1731 EST 3.36 down 0.00102 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_D80905_at D80905 1735 EST 3.59 down 0.0007
 D82061_at D82061 1741 Ke6 genem, mouse, human homoog of 6.1 down 0.00104
 D82422_at D82422 1745 ferroportin 1'; iron regulated gene 1 6.01 down 0.02351
 D85181-at D85181 1750 sterol-C5-desaturase (fungal ERG3, delta-5- 9.56 down 0.00005
 D86062_s_at D86062 1752 ES1 (zebrafish) protein, human homolog of 3.63 down 0.0001
 D87075_at D87075 1760 solute carrier family 23 (nucleobase transporters), 4.15 down 0.00067
 D87436_at D87436 1761 KIAA0249 gene product 5.49 down 0.00333
 D87449_at D87449 1762 KIAA0260 protein 4.58 down 0.00026
 D87466_at D87466 1763 KIAA0276 protein 4.83 down 0.0007
 D90042_at D90042 1767 N-acetyltransferase 2 (arylamine N- 7.06 down 0
 D90282_at D90282 1769 carbamoyl-phosphate synthetase 1, mitochondrial 27.29 down 0.00002
 rc_F02028_at F02028 1774 EST 23.48 down 0.00465
 rc_F02094_at F02094 1775 ecotropic viral integration site 5 3.41 down 0.0495
 rc_F02245_at F0-2245 1776 monoamine oxidase A 3.9 down 0.02943
 rc_F02345_at F02345 1779 EST 3.9 down 0.0033
 rc_F03200_at F03200 1783 EST 3.75 down 0.01805
 matrix metalloproteinase 2 (gelatinase A, 72kD
 rc_F03969_at F03969 1785 gelatinase, 72kD type IV collagenase) 7.87 down 0.00014
 rc_F04335_at F04335 1787 EST 3.16 down 0.0058
 rc_F04611_at F04611 1792 EST 23.96 down 0.00018
 rc_F04944_s_at F04944 1795 acyl-Coenzyme A oxidase 4.01 down 0.00242
 rc_F088170-at F08817 1796 EST 8.29 down 0.0077
 rc_F08941_at F08941 1798 EST 3.48 dosn 0.00428
 rc_F09058_at F09058 1799 EST 3.6 down 0.00595
 rc_F09350_at F09350 1801 EST 4.79 down 0.00088
 rc_F09353_at F09353 1802 solute carrier family 5 (inositol transporters), 3.3 down 0.02841
 core-binding facotr, runt domain, alpha subunit 2 ;
 rc_F09578_at F09578 1804 translocated to, 3 4.66 down 0.04463
 rc_F09979_at F9979 1809 EST 4.36 down 0.02555
 rc_F10182_s_at F10182 1812 hepsin (transmembrane protease, serine 1) 58.92 down 0.00837
 rc_F10276_s_at F10276 1814 dual specificity phosphatase 6 8.13 down 0.0001 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_F10466_at F10466 1820 EST 5.32 down 0.02494
 rc_F10640_at F10640 1821 EST 3.58 down 0.00152
 rc_F10874_f_at F10874 1823 EST 4.19 down 0.00025
 rc_F10875_at F10875 1824 EST 5.09 down 0.0004
 rc_F13702_at F13702 1826 EST 6.01 down 0.00064
 rc_F13782_s_at F13782 1827 LIM binding domain 2 4.17 down 0.00109
 TEK tyrosine kinase, endothelial (venous
 rc_H02848-s-at H02848 1831 malformations, multiple cutaneous and mucosal) 3.47 down 0.089
 rc_H02855_at H02855 1832 EST 5.96 down 0.00458
 rc_H03348_at H03348 1833 claudin 1 5.77 down 0.0001
 rc_H03945_at H03945 1835 EST 4.94 down 0.02603
 rc_H04142_f_at H04142 1836 EST 3.57 down 0.01906
 rc_H04242_at H04242: 1837 RAB5B, member RAS oncogene family 3.27 down 0.04826
 H04854_at H04854 1842 interleukin 1 receptor accessory protein 6.58 down 0.00007
 rc_H05072_at H05072 1843 EST 3.12 down 0.01248
 rc_H05974_s_at H05974 1850 EST 6.28 down 0.0549
 rc_H05985_at H05985 1851 hypothetical protein 6.43 down 0.04887
 rc_H06063_s_at H06063 1852 chondrotin sulfate proteoglycan 3 (neurocan) 3.15 down 0.00599
 rc_H06144_at H06144 1853 EST 3.1 down 0.00745
 rc_H06166_at H06166 1854 EST 3.31 down 0.03778
 rc_H06935_s_at H06935 1855 electron-transferring-flavoprotein dehydrogenase 6.82 down 0.00105
 rc_H08054_at H08054 1857 EST 4.2 down 0.0009
 rc_H08102_at H08102 1858 breast cell glutaminase 27.77 down 0.00032
 rc_H09167_at H09167 1860 KIAA0195 gene product 3.31 down 0.00313
 rc_H09353_at H09353 1866 EST 23.06 down 0.00094
 H09364_s_at H09364 1867 succinats dehydrogenase complex, subunit A, 5.74 down 0.03125
 rc_H09594-at H09594 1868 EST 3.12 down 0.00231
 rc_H09959_s_at H09959 1869 choline kinase 3.25 down 0.00225
 H10482_at H10482 1870 EST 3.19 down 0.01611
 rc_H10661_at H10661 1871 EST 4.54 down 0.00276 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change

Direction Pvalue
 methylenetetrahydrofolate dehydrogenase
 (NADP+ dependent), methenyltetrahydrofolate
 rc_H10779_s_at H10779 1872 cyclohydrolase, formyltetrahydrofolate synthetase 9.73 down 0.00035
 rc_H11274_at H11274 1874 EST 4.13 down 0.01478
 glycine dehydrogenase (decarboxylating; glycine
 rc_H11739_s_at H11739 1876 decarboxylase, glycine cleavage system protein 10.33 down 0.00023
 rc_H11746_at H11746 1877 EST 3.92 down 0.00012
 rc_H12257_at H12257 1879 EST 3.19 down 0.0069
 rc_H12593_at H12593 1880 zinc-finger protein 265 10.72 down 0.0056
 rc_H13696_at H13696 1882 EST 3.46 down 0.01796
 rc_H14372_s_at H14372 1883 ATP_binding cassette, sub-family A (ABC1), 5.16 down 0.00012
 rc_H16768_at H16768 1887 EST 3.72 down 0.00688
 rc_H18950_at H18950 1892 EST 3.85 down 0.00162
 rc_H18997_at H18997 1893 F-box protein 21 3.87 down 0.00611
 rc_H19504_f_at H19504 1895 EST 3.13 down 0.04948
 rc_H20543_at H20543 1897 DKFZP586B1621 protein 31.03 down 0.00074
 rc_H25124_at H25124 1903 EST 3.65 down 0.00004
 rc_H25551_at H25551 1904 EST 3.54 down 0.00366
 rc_H25836_at H25836 1905 tumor necrosis factor (ligand) superfamily, 3.3 down 0.03125
 rc_H26417_at H26417 1906 EST 3.22 down 0.03672
 rc_H26763_at H26763 1907 EST 3.39 down 0.04188
 rc_H27330_at H27330 1909 EST 3.2 down 0.00067
 rc_H27442_s_at H27442 1910 erythrocyte membrane protein band 7.2 6.81 down 0.00083
 rc_H29568_at H29568 1914 EST 11.45 down 0.00058
 rc_H30270_at H30270 1915 EST 17.09 down 0.00001
 rc_H38246_s_at H38246 1917 EST 9.25 down 0.00157
 rc_H39119_at H39119 1919 EST 3.06 down 0.03349
 rc_H40149_at H4019 1921 KIAA0937 rotein 4.59 down 0.00112
 rc_H40424_s_at H40424 1922 butyrate response factor 1 (EGF-response factor 3.56 down 0.04066
 rc_H40534_at H40534 1923 EST 3.18 down 0.01381
 rc_H41084_at H41084 1924 EST 6.31 down 0.0227 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_H41280_at H41280 1925 EST 3.68 down 0.00455
 rc_H42053_s_at H42053 1927 EST 3.49 down 0.01057
 rc_H46001_at H46001 1931 EST 5.03 down 0.00563
 H46990_at H46990 1993 cytochrome P450, subfamily IIE (ethanol- 3.2 down 0.00095
 rc_H47391_at H47391 1935 EST 3.1 down 0.03807
 rc_H47838_at H47838 1936 carboxypeptidase B2 (plasma) 16.74 down 0.00002
 rc_H49415_at H49415 1938 EST 3.72 down 0.005
 rc_H51340_at H51340 1941 EST 3.73 down 0.02643
 rc_H54285_s_at H54285 1947 EST 5.14 down 0.00426
 rc_H55759_at H55759 1949 EST 11.52 down 0.00034
 4-nitrophenylphosphatase domain and non-
 rc_H56584_at H56584 1951 neuronal SNAP25-like 1 9.5 down 0
 rc_H57060-s_at H57060 1954 EST 30.98 down 0.01687
 rc_H57166_at H57166 1955 EST 60.76 down 0.00007
 rc_H57816_at H57816 1957 EST 4.41 down 0.00206
 protein phosphatase 2 (formerly 2A), regulatory
 rc_H57850_at H57850 1958 subunit A (PR 65), beta isoform 3.02 down 0.00123
 rc_H58673_at H58673 1959 EST 14.85 down 0.00005
 rc_h58692_s_at H58692 1960 formyltetrahydrofolate dehydrogenase 81.41 down 0
 rc_H59136-at 59136 1962 EST 8.64 down 0.00013
 rc_H59141_at H59141 1963 EST 3.12 down 0.00293
 rc_H60595_s_at H60-595 1966 progesterone binding protein 15.8 down 0.01078
 rc_H61295_s_at H61295 1968 CD4 antigen (p55) 10.71 down 0.00925
 rc_H62838_at H62838 1971 EST 3.09 down 0.03201
 rc_H63251_at H63251 1972 KIAA0606 protein; SCN Circadian Oscillatory 3.27 down 0.02455
 rc_H65650_at H65650 1976 EST 3.88 down 0.0083
 rc_H66367_at H66367 1977 EST 6.68 down 0.0001
 rc_H66840-at H66840 1978 EST 3.67 down 0.0143
 rc_H67094_at H67094 1979 EST 3.24 down 0.00075
 rc_H67840_at H67840 1980 EST 3.1 down 0.00528
 rc_H68097_at H68097 1982 EST 3.83 down 0.00797 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 H68953_at H68953 1985 tranferrin 6.4 down 0.00132
 rc_H69138_at H69138 1986 v-Ki-ras2 Kirsten rat sarcoma 2 viral oncogene 6.76 down 0.00142
 rc_H69565_at H69565 187 EST 4.11 down 0.00002
 rc_H70554_at H70554 1989 EST 10.99 down 0
 rc_H71169_at H71169 1992 putative protein similar to nessy (Drosophila) 4 down 0.00709
 glucan (1,4-alpha-), branching enzyme 1
 rc_H71861_s_at H71861 1993 (glycogen branching enzyme, Andersen disease, 5.97 down 0.00007
 rc_H73535-s_at H73535 1996 EST 6.89

down 0.00202
 rc_H74317_s_at H74317 1997 apolipoprotein-A-II 45.09 down 0.01982

 rc_H77597_f_at H77597 2000 metallothionein 1H 16.03 down 0.00675
 H78628_at H78628 2003
 EST 4.98 down 0.00729
 rc_H79820_at H79820 2004 EST 3.25 down 0.01466

 rc_H80901_s_at H80901 2005 ficolin (collagen/fibrinogen domain-containing) 3 50.61 down
 0.00262
 rc_H81070_f_at H81070 2006 RNA helicase-related protein 25.74 down 0.00126

 rc_H82966_s_at H82966 2011 apolipoprotein B (including Ag(x) antigen) 3.42 down 0.00769

 rc_H83109-f_at H83109 2012 EST 16.55 down 0.00001
 rc_H83442_s_at H83442 2013
 catechol-O-methyltransferase 3.99 down 0.00594
 rc_H83451_at H83451 2014 EST 3.35 down
 0.00498
 rc_H87144_at H87144 2016 EST 3.41 down 0.00387
 rc_H87765_at H87765 2017
 KIAA0626 gene product 3.86 down 0.00131
 H88033_s_at H88033 2019 KIAA0733 protein 4.42
 down 0.02032
 rc_H88359_s-at H88359 2020 nuclear factor (erythroid-derived 2)-like 2 5.16
 down 0.01253
 rc_H88675_at H88675 2022 EST 5.63 down 0.00554
 rc_H89514_s_at
 H89514 2023 protein kinase, cAMP-dependent, catalytic, alpha 3.44 down 0.00435
 rc_H99893_at
 H99893 2025 EST 3.17 down 0.00658
 rc_H89980_at H89980 226 protein phosphatase 1,
 regulatory (inhibitor) 31.13 down 0.00006
 rc_H90417_s_at H90417 2028 EST 4.17 down
 0.015
 rc_H91325-s_at H91325 2029 aldolase B, fructose-bisphosphate 45.85 down 0.00505

 rc_H91456_s-at H91456 2030 nuclear receptor subfamily 1, group H, member 4 4.9 down
 0.00255
 phosphorylase, glycogen; liver (Hers disease,
 rc_H91680-s_at H91680 2032
 glycogen storage disease type VI) 4.15 down 0.00746 Table 6B. Down regulated in metastatic cancers
 versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change
 Direction Pvalue
 glutamate-cysteine ligase (gamma-
 rc_H93053_s_at H93053 2034
 glutamylcysteine synthetase), catalytic (72.8kD) 5.06 down 0.01029
 rc_H93246_s_at H93246
 2035 EST 15.3 down 0.0023
 rc_H93381_at H93381 2036 EST 24.23 down 0
 rc_H3562_at
 H93562 2038 proline synthetase co-transcribed (bacterial 3.17 down 0.0113
 3-hydroxy-3-
 methylglutaryl-Coenzyme A synthase
 rc_H94247_s_at H94247 2041 2 (mitochondrial) 9.49
 down 0.02373
 rc_H94475_s_at H94475 2043 alpha-2-plasmin inhibitor 40.92 down
 0.00271
 rc_H94648_at H94648 2044 EST 4.77 down 0.00266
 rc_H94666_at H94666 2045
 alpha-1-B glycoprotein 47.03 down 0.01158
 rc_H95358_at H95358 2049 EST 3.17 down
 0.00182
 rc_H95569_i_at H95569 2051 DKFZP586A0522 protein 28.48 down 0.00139

 rc_H95978_at H95978 2052 EST 8.55 down 0.00046
 rc_H96614_at H96614 2054 EST 4.02
 down 0.01565
 rc_H97868_at H97868 2064 EST 3.86 down 0.00362
 rc_H97986_at H97986
 2065 EST 3.86 down 0.01534
 rc_H98071_at H98071 2066 EST 4.66 down 0.03722

 rc_H98083_at H98083 2067 EST 5.09 down 0.00025
 rc_H98771_i_at H98771 2069
 BCL2/adenovirus E1B 19kD-interacting protein 8 down 0.0018
 rc_H98822_at H98822 2070 EST
 3.31 down 0.00174
 rc_H98910_s_at H98910 2071 EST 4.38 down 0.00548
 rc_H98977_at
 H98977 2073 EST 3.57 down 0.00298
 rc_H99393_s_at H99393 2076 endothelin receptor type B
 3.43 down 0.00093
 rc_H99727_at H99727 2080 adipose differentiation-related protein;
 adipophilin 5.83 down 0.04346
 rc_H99935_s-at H99935 2085 interleukin 6 signal transducer
 (gp130, oncostatin 3.59 down 0.00366 Table 6B. Down regulated in metastatic cancers versus normal
 sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction
 Pvalue
 J02843_at J02843 2088 cytochrome P450, subfamily IIE (ethanol- 22.58 down
 0.00935
 J002888_at J02888 2089 NAD(P)H menadione oxidoreductase 2, dioxin- 3.15 down
 0.02385
 J02943_at J02943 2090 corticosteroid binding globulin 18.98 down 0.00087

 J03242_s_at J03242 2092 insulin-like growth factor 2 (somatomedin A) 4.01 down 0.00042

 J03507_at J03507 2095 complement component 7 3.77 down 0.00184
 J03764_at J03764 2097
 plasminogen activator inhibitor, type I 5.6 down 0.02196
 protein phosphatase 2 (formerly 2A),
 catalytic
 J03805_s_at J03805 2098 subunit, beta isoform 3.87 down 0.0116
 J03810_at
 J03810 2099 solute carrier family 2 (facilitated glucose 21.99 down 0.00004
 J03910_ma1_at
 J03910 2101 EST 12.42 down 0.01167
 methylenetetrahydrofolate dehydrogenase
 (NADP+
 dependent), methylenetetrahydrofolate
 J04031_at J04031 2103 cyclohydrolase,
 formyltetrahydrofolate synthetase 3.4 down 0.00786
 J04056_at J04056 2104 carbonyl reductase 1

5.19 down 0.00001
 J04080_at J04080 2105 complement component 1, s subcomponent 5.48 down 0.0239
 J04093_s_at J04093 2106 UDP glycosyltransferase 1 18.92 down 0 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 J04093_s_at J04093 2106 UDP glycosyltransferase 1 18.92 down 0
 cytochrome P450, subfamily IIIA (niphedipine
 J04449_at J04449 2110 oxidase), polypeptide 3 5.25 down 0.01583
 J04615_at J04615 2112 SNRPN upstream reading frame 3.14 down 0.02928
 syndecan 2 (heparan sulfate proteoglycan 1, cell
 J04621_at J04621 2113 surface-associated fibroglycan) 3.38 down 0.00275
 cytochrome P450, subfamily IIIA (niphedipine
 J04813_s_at J04813 2114 oxidase), polypeptide 5 9.67 down 0.0107
 J05037_at J05037 2116 serine dehydratase 16.24 down 0.00015
 J05158_at J05158 2117 carboxypeptidase N, polypeptide 2, 83kD 8.52 down 0
 J05428_at J05428 2120 UDP glycosyltransferase 2 family, polypeptide B7 16.14 down 0.00563
 K02100_at K02100 2123 ornithine carbamoyltransferase 10.24 down 0.00009
 K02215_at K02215 2124 angiotensinogen 16.51 down 0.00006
 coagulation factor IX (plasma thromboplastic
 K02402_at K02402 2125 compoent, Christmas disease, hemophilia B) 28.81 down 0.00001
 K02766_at K02766 2126 complement component 9 21.24 down 0
 cytochrome P450, subfamily IIA (phenobarbital-
 K03192_f_at K03192 2127 inducible), polypeptide 6 69.92 down 0
 cytochrome P450, subfamily IIA (phenobarbital-
 K03192_f_at K03192 2127 inducible), polypeptide 6 50.16 down 0
 L00190_s_at L00190 2130 antithrombin III 42.41 down 0.00012
 L00352_at L00352 2131 low density lipoprotein receptor (familial 4.19 down 0.00352
 L00972_at L00972 2133 cystathionine-beta-synthase 7.19 down 0.00008
 L04751_at L04751 2138 cytochrome P450, subfamily IVA, polypeptide 11 36.79 down 0.00004
 L05144_at L05144 2139 phosphoenolpyruvate carboxykinase 1 (soluble) 4.76 down 0.02289
 L05779_at L05779 2140 epoxide hydrolase 2, cytoplasmic 5.35 down 0.00006
 3-hydroxymethyl-3-methylglutaryl-Coenzyme A
 L07033_at L07033 2144 lyase (hydroxymethylglutaricaciduria) 3.49 down 0
 enoyl-Coenzyme A, hydratase/3-hydroxyacyl
 L07077_at L07077 2145 Coenzyme A dehydrogenase 4.82 down 0.00403
 L07765_at L07765 2147 carboxylesterase 1 (monocyte/macrophage 20.53 down 0.00025 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank seq ID Known Gene Name Fold Change Direction Pvalue
 glucan (1,4-alpha-), branching enzyme 1
 L07956_at L07956 2148 (glycogen branching enzyme, Andersen disease, 5.6 down 0.00029
 fatty-acid-Coenzyme A ligase, long-chain 1,fatty-
 L09229_s_at L09229 2150 acid-Coenzyme A ligase, long-chain 2 18.34 down 0.00016
 L09708_at L09708 2152 complement component 2 3.92 down 0.00693
 L09717_at L09717 2153 lysosomal-associated membrane protein 2 4.06 down 0.00034
 L11005_at L11005 2154 aldehyde oxidase 1 16.3 down 0.00065
 L11244_s_at L11244 2155 complement component 4-binding protein, beta 43.33 down 0
 L11244_s_at L11244 2155 complement component 4-binding protein, beta 12.03 down 0.0001
 L11708_at L11708 2158 hydroxysteroid (17-beta) dehydrogenase 2 5.99 down 0.01516
 L11931_at L11931 2159 serine hydroxymethyltransferase 1 (soluble) 7.27 down 0.00041
 L12760_s_at L12760 2162 phosphoenolpyruvate carboxykinase 1 (soluble) 12.75 down 0.00035
 L13278_at L13278 2163 crystallin, zeta (quinone reductase) 5.83 down 0.0034
 L15702_at L15702 2165 B-factor, properdin 3.7 down 0.04693
 cytochrome P450, subfamily IIC (mephenytoin 4-
 L16883_s_at L16883 2166 hydroxylase), polypeptide 9 84.71 down 0.00327
 L17128_at L17128 2167 gamma-glutamyl carboxylase 4.02 down 0.00096
 phosphodiesterase 4A, cAMP-specific (dunce
 L20965_at L20965 2175 (Drosophila)-homolog phosphodiesterase E2) 3.02 down 0.01177
 solute carrier family 10 (sodium/bile acid
 L21893_at L21893 2176 cotransporter family), member 1 13.18 down 0.00155
 L22548_at L22548 2178 collagen, type XVIII, alpha 1 3.87 down 0.0299
 L25878_s_at L25878 2183 epoxide hydrolase 1, microsomal (xenobiotic) 26.84 down 0
 L25880_s_at L25880 2184 epoxide hydrolase 1, microsomal (xenobiotic) 58.7 down 0.00013
 L27050_at L27050 2186 apolipoprotein F 10.26 down 0.00026
 L29008_at L29008 2189 sorbitol dehydrogenase 3.51 down 0.00825
 L29433_at L29433 2191 coagulation factor X 7.74 down 0.00244
 L32140_at L32140 2192 afamin 17.31 down 0.00003
 L32179_at

L32179 2193 arylacetamide deacetylase (esterase) 23.83 down 0
 bile acid Coenzyme A: amino acid N-
 L34081_at L34081 2199 acyltransferase (glycine N-choloyltransferase) 11.96 down 0.00008 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 glutamate-cysteine ligase (gamma-
 L35546_at L35546 2203 glutamylcysteine synthetase), regulatory (30.8kD) 14.18 down 0.00018
 glutamate-cysteine ligase (gamma-
 L35546_at L35546 2203 glutamylcysteine synthetase), regulatory (30.8kD) 5.56 down 0.0005
 L36033_at L36033 2204 stromal cell-derived factor 1 5.1 down 0.00603
 L38490_s_at L38490 2207 AdP-ribosylation factor 4-like 3.13 down 0.01306
 5,10-methenyltetrahydrofolate synthetase (5-
 L38928_at L38928 2209 formyltetrahydrofolate cyclo-ligase) 10.97 down 0.0267
 5,10-methenyltetrahydrofolate synthetase (5-
 L38928_at L38928 2209 formyltetrahydrofolate cyclo-ligase) 5.17 down 0.00726
 L40401_at L40401 2211 putative protein 6.97 down 0.00079
 L40401_at L40401 2211 putative protein 4.26 down 0.00194
 L41067_at L41067 2213 nuclear factor of activated T-cells, cytoplasmic 3 4.96 down 0.00473
 L47726_at L47726 2219 phenylalanine hydroxylase 25.63 down 0.00019
 L48516_at L48516 2220 paraoxonase 3 22.21 down 0.00004
 L49169_at L49169 2221 FBJ murine osteosarcoma viral oncogene 3.4 down 0.01193
 L76465_at L76465 2224 hydroxyprostaglandin dehydrogenase 15-(NAD) 3.56 down 0.00688
 L76571_at L76571 2226 nuclear receptor subfamily 0, group B, member 2 4.44 down 0.00312
 L76687_at L76687 2227 growth factor receptor-bound protein 14 5.16 down 0.00199
 L76927_rna1_at L76927 2228 galactokinase 1 3.66 down 0.00999
 solute carrier family 25 (mitochondrial carrier;
 L77567_s_at L77567 2229 citrate transporter), member 1 3.14 down 0.04095
 M10058_at M10058 2230 asialoglycoprotein receptor 1 23.96 down 0
 M10612_at M10612 2232 apolipoprotein C-II 17.13 down 0.00746
 M10942_at M10942 2233 metallothionein 1E (functional) 6.19 down 0.00428
 M10943_at M10943 2234 metallothionein 1F (functional) 3.88 down 0
 M11025_s_at M11025 2235 asialoglycoprotein receptor 2 17.56 down 0.00003
 M11313_s_at M11313 2236 alpha-2-macroglobulin 10.05 down 0.00014
 M11321_at M11321 2237 group-specific component (vitamin D binding 16.52 down 0.01416
 M11437_cds1_at M11437 2238 kininogen 18.38 down 0.00006
 M11437_cds2_at M11437 2238 kininogen 16.19 down 0.02277 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 M11567_rna1_at M11567 2239 angiogenin, ribonuclease, RNase A family, 5 32.25 down 0.0001
 M12174_at M12174 2242 ras homolog gene family, member B 5.44 down 0.0088
 alcohol dehydrogenase 1 (class I), alpha
 polypeptide, alcohol dehydrogenase 2 (class I),
 M12272_s_at M12272 2243 beta polypeptide, alcohol dehydrogenase 3 (class 32.42 down 0.0034
 M12529_at M12529 2244 apolipoprotein E 3.05 down 0.03776
 M12625_at M12625 2245 lecithin-cholesterol acyltransferase 4.55 down 0.01584
 M12712_s_at M12712 2246 protein C (inactivator of coagulation factors Va 7.37 down 0.01866
 alcohol dehydrogenase 1 (class I), alpha
 polypeptide, alcohol dehydrogenase 2 (class I),
 M12963_s_at M12963 2248 beta polypeptide, alcohol dehydrogenase 3 (class 48.95 down 0.00104
 M13143_at M13143 2249 kallikrein B plasma, (Fletcher factor) 1 10.39 down 0.00019
 M13149_at M13149 2250 histidine-rich glycoprotein 18.65 down 0.02974
 M13232_s_at M13232 2251 coagulation factor VII (serum prothrombin 5.9 down 0.00014
 M13690_s_at M13690 2252 complement component 1 inhibitor (angioedema, 6.07 down 0.00045
 M13699_at M13699 2253 ceruloplasmin (ferroxidase) 15.85 down 0.00012
 M13829_s_at M13829 2254 v-raf murine sarcoma 3611 viral oncogene 6.52 down 0
 M14058_at M14058 2256 complement component 1, r subcomponent 6.66 down 0.00229
 M14091_at M14091 2257 thyroxine-binding globulin 10.66 down 0.00024
 M14218_at M14218 2259 argininosuccinate lyase 9.03 down 0.00078
 M14338_at M14338 2260 protein S (alpha) 12.33 down 0
 phosphorylase, glycogen; liver (Hers disease,
 M14636_at M14636 2262 glycogen storage disease type VI) 3.45 down 0.00133
 M15465_s_at M15465 2266 pyruvate kinase, liver and RBC 6.1 down 0.00069
 M15517_cds5_at M15517 2267 EST 22.76 down 0.03365
 M15656_at M15656 2268 aldolase B, fructose-bisphosphate 96.66 down 0
 M16447_at M16447 2270 quinoid

dihydropteridine reductase 6.57 down 0.00015
 M16474_s_at M16474 2271 butyrylcholinesterase
 5.82 down 0.00113
 M16594_at M16594 2272 glutathione S-transferase A2 73.21 down 0

 M16750_2_at M16750 2273 pim-1 oncogene 3.08 down 0.01811
 M16961_at M16961 2274
 alpha-2-HS-glycoprotein 21.45 down 0.01175 Table 6B. Down regulated in metastatic cancers versus
 normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction
 Pvalue
 M16967_at M16967 2275 coagulation factor V (proaccelerin, labile factor) 5.56 down
 0.00047
 M16973_at M16973 2276 complement component 8, beta polypeptide 22.75 down
 0.00001
 M16974_s_at M16974 2277 complement component 8, alpha polypeptide 49.47 down
 0.00046
 M17262_at M17262 2278 coagulation factor II (thrombin) 44.3 down 0.00345

 M17262_at M17262 2278 coagulation factor II (thrombin) 14.24 down 0.00028
 M17466_at
 M17466 2279 coagulation factor XII (Haegman factor) 9.76 down 0.00285
 dystrophin (muscular
 dystrophy, Duchenne and
 Becker types), includes DXS142, DXS164,
 M18533_at M18533
 2284 DXS206, DXS230, DXS239, DXS268, DXS269, 3.45 down 0.00313
 M19828_s_at M19828
 2287 apolipoprotein B (including Ag(x) antigen) 29.37 down 0.00137
 M20218_at M20218 2288
 coagulation factor XI (plasma thromboplastin 6.4 down 0.00004
 M20786_at M20786 2290 alpha-
 2-plasmin inhibitor 16.95 down 0.00709
 M20867_s_at M20867 2291 glutamate dehydrogenase 1
 17.73 down 0.00002
 M20902_at M20902 2292 apolipoprotein C-I 3.14 down 0.0389

 M21642_at M21642 2294 antithrombin III 15.82 down 0.01027
 M21642_s_at M21642 2294
 antithrombin III 15.23 down 0.02088
 M22976_at M22976 2297 cytochrome b-5 7.39 down
 0.02431
 M23161_at M23161 2298 EST 3.44 down 0.00733
 M23234_s_at M23234 229
 ATP-binding cassette, sub-family B (MDR/TAP), 10.05 down 0
 androgen receptor
 (dihydrotestosterone receptor;
 testicular feminization; spinal and bulbar
 M23263_at
 M23263 2300 muscular atrophy; Kennedy disease) 4.6 down 0.00005
 androgen receptor
 (dihydrotestosterone receptor;
 testicular feminization; spianl and bulbar
 M23263_s_at
 M23263 2300 muscular atrophy; Kennedy disease) 3.35 down 0.02551
 intercellular adhesion
 molecule 1 (CD54), human
 M24283_at M24283 2303 rhinovirus receptor 3.19 down
 0.04985
 M25079_s_at M25079 2305 hemoglobin, beta 9.15 down 0.01399
 M25280_at
 M25280 2306 selectin L (lymphocyte adhesion molecule 1) 3.39 down 0.004
 M26393_s_at
 M26393 2309 acyl-Coenzyme A dehydrogenase, C-2 to C-3 16.27 down 0.00007
 M27492_at
 M27492 2312 interleukin 1 receptor, type I 4.62 down 0.0082 Table 6B. Down regulated in metastatic
 cancers versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold
 Change Direction Pvalue
 M29194_at M29194 2315 lipase, hepatic 12.18 down 0.00012

 M29873_s_at M29873 2318 cytochrome P450, subfamily IIB (phenobarbital- 56.71 down 0.0054

 M29874_s_at M29874 2319 cytochrome P450, subfamily IIB (phenobarbital- 18.44 down
 0.00081
 M29971_at M29971 2320 O-6-methylguanine-DNA methyltransferase 3.97 down
 0.00424
 M30185_at M30185 2321 cholesteryl ester transfer protein, plasma 3.83 down
 0.0013
 M30185_at M30185 2321 cholesteryl ester transfer protein, plasma 3.39 down
 0.00089
 M30257_s_at M30257 2322 vascular cell adhesion molecule 1 3.11 down 0.00064

 M30269_at M30269 2323 nidogen (enactin) 3.4 down 0.00026
 M31169_s_at M31169 2325
 propionyl Coenzyme A carboxylase, beta 4.65 down 0.00467
 M31627_at M31627 2330 X-box
 binding protein 1 6.97 down 0.00052
 cytochrome P450, subfamily I (aromatic
 M31667_f_at
 M31667 2331 compound-inducible), polypeptide 2 4.38 down 0.00078
 M31994_at M31994 2332
 aldehyde dehydrogenase 1, soluble 11.24 down 0.01192
 cytochrome P450, subfamily IIA
 (phenobarbital
 M33317_f_at M33317 2338 inducible), polypeptide 7 32.63 down 0

 cytochrome P450, subfamily IIA (phenobarbital
 M3318_r_at M33318 2339 inducible),
 polypeptide 6 3.21 down 0.01621
 M34276_at M34276 2341 plasminogen 24.73 down
 0.00031
 M35410_s_at M35410 2344 insulin-like growth factor binding protein 2 (36kD) 6.45
 down 0.04517
 MIP-B_at M35590 2345 small inducible cytokine A4 5.96 down 0.01225

 MIP-B_at M35590 2345 small inducible cytokine A4 4.74 down 0.01225
 MIP-B_at M35590
 2345 small inducible cytokine A4 4.62 down 0.01268
 M35878_at M35878 2346 insulin-like
 growth factor binding protein 3 4.3 down 0.0027
 glutamix-oxaloacetic transaminase 1,

soluble
 M37400_at M37400 2348 (aspartate aminotransferase 1) 8.7 down 0.0004
 M55150_at M55150 2352 fumarylacetoacetate 3.93 down 0.00213
 potassium voltage-gated channel, shaker-related
 M55513_s_at M55513 2354 subfamily, member 5 4.81 down 0.02141
 M55671_at M55671 2355 protein Z, vitamin K-dependent plasma 4.74 down 0.00078
 M57731_s_at M57731 2359 GRO2 oncogene 13.87 down 0.0123
 M58286_s_at M58286 2360 tumor necrosis factor receptor superfamily, 8.15 down 0.00037 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 M58569_s_at M58569 2361 EST 16.15 down 0.00174
 M58600_ma1_at M58600 2362 heparin cofactor II 39.79 down 0.00034
 tissue factor pathway inhibitor (lipoprotein-
 M59499_at M59499 2363 associated coagulation inhibitor) 5.92 down 0.0005
 M59815_at M59815 2364 complement component 4A 8.02 down 0.00049
 sphingomyelin phosphodiesterase 1, acid
 M59916_at M59916 2365 lysosomal (acid sphingomyelinase) 3.36 down 0.0038
 M60974_s_at M60974 2368 growth arrest and DNA-damage-inducible, alpha 3.48 down 0.00209
 cytochrome P450, subfamily IIC (mephenytoin 4-
 M61853_at M61853 2369 hydroxylase), polypeptide 18 7.82 down 0.00024
 M61854_s_at M61854 2370 cytochrome P450, subfamily IIC (mephenytoin 4- 3.3 down 0.04185
 cytochrome P450, subfamily IIC (mephenytoin 4-
 M61855_at M61855 2371 hydroxylase), polypeptide 9 38.82 down 0.00023
 M62403_s_at M62403 2373 insulin-like growth factor-binding protein 4 4.12 down 0.00226
 M62486_at M62486 2374 complement component 4-binding protein, alpha 22.08 down 0.00272
 glutathione S-transferase M1, glutathione S-
 M63509_s_at M63509 2376 transferase M2 (muscle), glutathione S- 7.06 down 0.03887
 M63967_at M63967 2378 aldehyde dehydrogenase 5 4.04 down 0.00058
 M64554_ma1_at M64554 2380 coagulation factor XIII, B polypeptide 5.87 down 0.00011
 glycine dehydrogenase (decarboxylating; glycine
 M64590_at M64590 2381 decarboxylase, glycine cleavage system protein 6.41 down 0.00002
 M65131_ma1_at M65131 2384 methylmalonyl Coenzyme A mutase 7.44 down 0.00004
 M65134_s_at M65134 2385 complement component 5 12.01 down 0.00012
 M65292_s_at M65292 2386 H factor (complement)-like 1,H factor 1 7.56 down 0.01152
 M68516_ma1_at M68516 2387 protein C inhibitor (plasminogen activator inhibitor 20.54 down 0
 M68840_at M68840 2388 monoamine oxidase A 3.96 down 0.01396
 M68895_ma1_at M68895 2390 alcohol dehydrogenase 6 (class V) 4.25 down 0.00354
 M69177_at M69177 2392 monoamine oxidase B 11.64 down 0.00001
 M72885_ma1_s_at M72885 2393 putative lymphocyte G0/G1 switch gene 6.5 down 0.03461
 M74587_ma1_s_at M74587 2394 insulin-like growth factor binding protein 1 11.42 own 0.00274
 M75106_at M75106 2397 carboxypeptidase B2 (plasma) 40.63 down 0 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 M76665_at M76665 2398 hydroxysteroid (11-beta) dehydrogenase 1 19.22 down 0.00004
 M80482_at M80482 2304 paired basic amino acid cleaving system 4 4.26 down 0.00041
 M81182_s_at M81182 2404 ATP-binding cassette, sub-family D (ALD), 3.45 down 0.00499
 M81349_at M81349 2405 serum amyloid A4, constitutive 76.15 down 0.00015
 M83216_s_at M83216 2407 caldesmon 1 4.27 down 0.00037
 M83652_s_at M83652 2408 proterdin P factor, complement 6 down 0.0002
 M83772_at M83772 24098 flavin containing monooxygenase 3 19.54 down 0
 M86826_at M86826 2413 insulin-like growth factor binding protein, acid 3.75 down 0.01157
 M86873_s_at M86873 2414 plasminogen, plasminogen-like 17.54 down 0
 SWI/SNF related, matrix associated, actin
 M88163_at M88163 2416 dependent regulator of chromatin, subfamily a, 3.37 down 0.00098
 M91432_at M91432 2420 acyl-Coenzyme A dehydrogenase, C-4 to C-12 6.74 down 0.00008
 M92843_s_at M92843 2421 zinc finger protein homologous to Zfp-36 in 3.02 down 0.04958
 M93143_at M93143 2423 plasminogen-like 10.06 down 0.00098
 M93405_at M93405 2424 methylmalonate-semialdehyde dehydrogenase 23.06 down 0
 M94065_s_at M94065 2425 dihydroorotate hydrogenase 11.78 down 0.00034
 M94065_at M94065 2425 dihydroorotate dehydrogenase 6.47 down 0.00013
 M95585_s_at M95585 2430 hepatic leukemia factor 4.2 down 0.00212
 M95767_at M95767 2432 chitobiase, di-N-acetyl 4.94 down 0.0004
 glutathione S-

transferase M1, glutathione S-
 M96233_s_at M96233 2433 transferase M2 (muscle), glutathione S- 4.23 down 0.04227
 M96843_at M96843 2435 EST 8.42 down 0.02394
 M96843_at M96843 2435 EST 4.08 down 0.02912
 M99439_at M99439 2438 transducin-like enhancer of split 4, homolog of 5.14 down 0.00001
 rc_N20113_s_at N20113 2439 EST 5.24 down 0.01346
 rc_N21079_at N21079 2441 nucleolar cystein-rich protein 4.1 down 0.00028
 rc_N21550_at N21550 2444 EST 3.08 down 0.00006
 rc_N21646_at N21656 2446 EST 3.79 down 0.00079
 rc_N22404_at N21404 2450 EST 3.99 down 0.01152
 rc_N22434_at N21434 2451 EST 4.37 down 0.01725
 rc_N22854_s_at N22854 2452 CASP2 and RIPK1 domain containing adaptor 3.34 down 0.0084 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_N22938_s_at N22938 2453 serum amyloid A4, constitutive 35.39 down 0.00128
 rc_N23665_s_at N23665 2455 hydroxysteroid (17-beta) dehydrogenase 2 9.4 down 0.00055
 rc_N23730_s_at N23730 2456 v-fos FBJ murine osteosarcoma viral oncogene 4.38 down 0.04395
 rc_N23761_at N23761 2457 DKFZP586G011 protein 5.41 down 0.00448
 N23817_at N23817 2458 EST 3.76 down 0.00288
 rc_N24879_at N24879 2460 EST 9.44 down 0.00008
 rc_N25082_s_at N25082 2463 amplified in osteosarcoma 5.19 down 0.00895
 rc_N25193_at N25193 2464 EST 3.13 down 0.01955
 protein kinase, cAMP-dependent, regulatory, type
 rc_N25969_s_at N25969 2466 I, alpha (tissue specific extinguisher 1) 4.32 down 0.00304
 rc_N26184_at N26184 2467 MYLE protein 4.82 down 0.00056
 rc_N27524_at N27524 2472 EST 3.13 down 0.00216
 rc_N27563_at N27563 2473 EST 3.3 down 0.00021
 N27670_at N27670 2474 progesterone membrane binding protein 6.15 down 0.00321
 rc_N27834_at N27834 2475 alpha2,3-sialyltransferase 5.31 down 0.00039
 rc_N29319_at N29319 2476 EST 4.58 down 0.00011
 rc_N29353_at N29353 2477 kynurenine 3-monooxygenase (kynurenine 3- 4.78 down 0.00019
 rc_N30856_at N30856 2485 solute carrier family 19 (thiamine transporter), 3.71 down 0.00393
 rc_N31598_at N31598 2488 EST 3.1 down 0.00203
 rc_N31741_at N31741 2489 serien hydroxymethyltransferase 1 (soluble) 14.76 down 0.00001
 rc_N31952_at N31952 2490 est 3.13 down 0.01481
 rc_N32071_at N32071 2491 est 8.75 down 0.00006
 rc_N33009_s_at N33009 2492 apolipoprotein E 60.54 down 0.0093
 rc_N34441_at N34441 2496 EST 3.07 down 0.00186
 rc_N34804_at N34804 2497 DKFZP434J214 protein 8.08 down 0.00028
 rc_N36001_at N36001 2504 EST 6.16 down 0.00222
 rc_N36250_at N36250 2506 cellular repressor of E1A-stimulated genes 4.06 down 0.00776
 rc_N39163_at N39163 2509 metallothionein 1L 4.3 down 0.03917
 rc_N39201_at N39201 2510 protease inhibitor 4 (kallistatin) 24.91 down 0.000253
 rc_N40188_at N40188 2513 EST 3.72 down 0.01771
 N40320_at N40320 2514 est 7.56 DOWN 0.01584 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_N45232_at N45232 2517 EST 3.61 down 0.01308
 rc_N45307_s_at N45307 2518 EST 4.55 down 0.00006
 rc_N45998_at N45998 2520 EST 3.14 down 0.00337
 rc_N474689_at N47469 2522 EST 3.34 down 0.00329
 rc_N47942_at N47942 2523 progesterone membrane binding protein 4.51 down 0.00168
 rc_N48180_at N48180 2526 EST 3.36 down 0.00543
 rc_N48315_at N48315 2527 adaptor-related protein complex 2, mu 2 subunit 5.3 down 0.0149
 rc_N48602_at N48602 2529 EST 3.17 down 0.02913
 rc_N48674_at N48674 2530 EST 4.06 down 0.00028
 rc_N48787_at N48787 2531 protease inhibitor 1 (anti-elastase), alpha-1- 4.4 down 0.00292
 rc_N49090_at N49090 2533 EST 18 down 0.00501
 rc_N49104_s_at N49104 2534 nuclear receptor interacting protein 1 3.83 down 0.00144
 rc_N49113_at N49113 2535 EST 3.4 down 0.00162
 rc_N49214_at N49214 2536 EST 4.74 down 0.00064
 rc_N49595_at N49595 2538 EST 10.39 down 0.00022
 rc_N49902_at N49902 2540 EST 3.55 down 0.00455
 rc_N51117_at N51117 2544 EST 9.68 down 0.00081
 rc_N51737_at N51737 2547 mitogen-activated protein kinase kinase kinase 3.32 down 0.00376
 rc_N51773_at N51773 2549 EST 16.32 down 0.0007
 rc_N52271_at N52271 2552 LIM protein (similar to rat protein kinase C- 8.06 down 0.00011
 rc_N52322_at N52322 2553 EST 3.27 down 0.00933
 rc_N52845_at N52845 2554 EST 5.53 down 0.00088
 rc_N52985_at N52985 2555

nidogen (enactin) 4.21 down 0.01385
 rc_N53031_s_at N53031 2556 UDP glycosyltransferase 2 family, polypeptide B4 97.58 down 0.00022
 rc_N53352_at N53352 2558 EST 3.22 down 0.00416
 cytochrome P450 subfamily IIJ (arachidonic acid
 rc_N53549_s_at N53549 2559 epoxigenase) polypeptide 2 4.68 down 0.00818
 rc_N53757_at N53757 2560 EST 3.97 down 0.00255
 rc_N54053_at N54053 2561 secreted phosphoprotein 2, 24D 60.39 down 0.00087
 rc_N54311_at N54311 2564 EST 4.82 down 0.00183
 rc_N54399_at N54399 2566 EST 3.34 down 0.00048 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_N54417_s_at N54417 2567 fibrinogen, A alpha polypeptide 99.28 down 0.00001
 rc_N54429_at N54429 2568 EST4 57.81 down 0.00724
 rc_N54511_s_at N54511 2569 KIAA0265 protein 3.45 down 0.03362
 rc_N54604_at N54604 2570 EST 3.72 down 0.00741
 cytidine monophosphate-N-acetylneuraminic acid
 rc_N54792_at n54792 2571 hydroxylase (CMP-N-acetylneuroamate 3.23 down 0.00099
 rc_N54950_s_at N54950 2573 ketohexokinase (fructokinase) 17.17 down 0.00078
 N57464_at N57464 2576 CCAAT/enhancer binding protein (C/EBP), delta 14.69 down 0.00018
 rc_N57934_s_at N57934 2577 forminiminotrasferase cyclodeaminase 13.81 down 0.00171
 rc_N58326_at N58326 2579 EST 14.97 down 0.00647
 rc_N59089_at N59089 2581 EST 4.74 down 0.00055
 rc_N59231_s_at N59231 2582 pyruvate carboxylase 3.45 down 0.2066
 rc_N59283_at N5283 2583 EST 4.65 down 0.02343
 rc_N59474_at N59474 2584 EST 6.93 down 0.00337
 rc_N59532_s_at N59532 2585 ainomethyltransferase (glycine cleavage 6.73 down 0.00005
 rc_N59543_at N59543 2587 PDZ domaine containing 1 9.96 down 0.00052
 rc_N59550_at N59550 2588 EST 25.56 down 0.00024
 rc_N62443_at N62443 2590 EST3.72 down 0.01717
 rc_N62523_at N62523 2592 hepatic leukemia factor 5.02 down 0.00087
 rc_N62652_s_at N62652 2593 EST 5.23 down 0.03006
 rc_N63391_at N63391 2600 EST 7.39 down 0.00565
 rc_N63688_at n^3688 2603 EST 3.13 down 0.002
 rc_N63698_at N63698 2604 EST 7.92 down 0.00001
 rc_N63845_at N63845 2605 phytanoyl-CoA dhydroxylase (Refsum disease) 25.92 down 0.00084
 rc_N64017_at N64017 2606 EST 5.27 down 0.00022
 enoyl-Coenzyme A, hydratase/3-hydroxyacyl
 rc_N64036_s_at N64036 2607 Coenzyme A dehydrogenase 9.99 down 0.00125
 rc_N64436_at N64436 2609 EST 3.51 down 0.00441
 rc_N64535_at N64535 2610 EST 6.19 down 0.00106
 rc_N65959_at4 N65959 2612 EST 5.43 down 0.00044
 rc_N66066_at N66066 2613 EST 28.35 down 0.00055 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction pvalue
 rc_N66130_at N66130 2614 progesterone membrane binding protein 3.98 down 0.0106
 rc_N66422_at N66422 2616 EST 4.1 down 0.00237
 rc_N66763_at N66763 2619 EST 3.79 down 0.03015
 rc_N66857_at4 N66857 2620 EST 15.03 down 0.00005
 prion protein (p27-30) (Creutzfeld-Jakob disease,
 rc_N67009_s_at N67009 2622 Gerstmann Strausler-Scheinker syndrome, fatal 3.55 down 0.00956
 rc_N67096_at N67096 2623 EST 3.23 down 0.00446
 rc_N67105_at N67105 2624 EST 5.01 down 0.00176
 rc_N67378_at N67378 2626 KIAA1053 protein 7.14 down 0
 re_N67876_s_at N67876 2628e insulin-like growth factor 1 (somatomedin C) 8.89 down 0.00042
 rc_N67893i_at N67893 2629 EST 10.48 down 0.00341
 rc_N68596_s_at4 N68596 2636 betain-homocysteine methyltransferase 40.99 down 0
 rc_N68730_at N68730 2637 EST 3.88 down 0.00091
 rc_N68974_at N68974 2640 EST 16.44 down 0.00087
 rc_N68993_at n68993 2641 EST 3.06 down 0.00867
 rc_N69136_at N69136 2645 EST 18.53 down 0.00366
 rc_N69216_at N69216 2646 EST 3.4 down 0.00497
 rc_N69299_at N69299 2649 EST 3.63 down 0.03776
 rc_N70005_at N70005 2653 EST 3.42 down 0.04229
 rc_N70057_s_at4 N70057 2654 DNA segment on chromosome 6 (unique) 49 5.24 down 0.01178
 rc_N70305_at N70305 2655 EST 4.41 down 0.00078
 rc_N70358_s_at N70358 2657 growth hormone receptor 34.35 down 0
 rc_N70861_at N70861 2661 EST 6.55 down 0.00001
 solute carrier faily 10 9sodium/bile acid
 rc_N70966_s_at N70966 2663 co4transporter family), member 1 34.06 down 0.0006
 rc_N71542-at N71542 2665 kidney-and live-specific gene 21.05 down0
 rc_n71935_s_at N71935 2667 multiple PDZ domain protein 16.28 down 0
 rc_N72259_at N72259

2670 cornichon-lie 4.65 down 0.0054
 rc_N76295_s_at N72695 2671 EST 9.18 down 0.00069
 rc_N73461_f_at N73461 2673 EST 4.25 down 0.00162
 rc_N73468_s_at N73468 2674 protein S (alpha) 4.4 down 0.00853 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_N73543-at N73543 2675 EST 17 down 0.00003
 rc_N73561_at4 N73561 2676 Est 12.96 down 0.00011
 rc_N73883i_at N73883i 2682 EST 9.35 down 0
 rc-N73998_at N73988 2683 EST 10.27 down 0.00083
 rc_N74025_at N74025 2685 deiodinase, iodothyronine, tyep I 22.79 down 0
 rc_N74422-at N74422 2686 EST 30.32 down 0
 rc_N74558_at N74558 2687 EST 3.19 down 0.00247
 rc_N75072_at4 N75072 2689 EST 3.73 down 0.00379
 n75203_s_at N75203 2691 EST 6.15 down 0.00181
 N75870_s_at N75870 2693 dual specicity phosphatase 1 13.41 down 0.00251
 rc_N76012_r-at N76012 e2694 EST 36.71 down 0.00598
 N77326_at N77326 2696 EST 7.51 down 0.00542
 N77606_at N77606 2697 EST 4.22 down 0.00119
 macrophage stimulating 1 (hepatocyte growth
 rc_N788i50_s_at N78850 2699 factor-like), macrophage stimulation, pseudogene 13.69 down 0.00421
 rc_N78902i_at N789022 2700 leptin receptor 6.79 down 0.0041
 rc_N79435-at N79435 2701 chronosome 15 open reading frame 3 3.73 down 0.00861
 rc_N79778_at N79778 2702 extracellular matrix protein 2, female organ and 5.15 down 0.00286
 rc_N80129_i_at N80129 2703 metallotioine 1L 66.48 down 0.00415
 rc_N8I0129_f_at N80129 2703 metallothionein 1L 13.6 down 0.00196
 rc_N81025_at N81025 2705 EST 8.61 down 0.00015
 rc_n81036_at4 N81036 2706 EST 6.89 down 0.00276
 N89302_s_at N89302 2708 HLA-B associated transcript-3 23.44 down 0.00192
 rc_N89738_at N89738 2710 Est 10.06 down 0.00052
 rc_N90584_at N90584 2714 EST 3.08 down 0.02602
 N90820_at N90820 2715 DKFZP566B1346 protein 4.86 down 0.03008
 N91087_at N91087 2717 EST 6.91 down 0.00109
 rc_N91273_r_at N91273 2718 EST 4.07 down 0.02965
 rc_N91882_at N91882 2720 alpha2,3-sialyltransferase 14.52 down 0.00024
 rc_N93155_f_at N93155 2729 clamodulin 1 (Phosphorylase kinase, delta) 4.39 down 0.0002
 rc_N93155_i_at N93155 2729 calmodulin 1 (Phosphorylase kinase, delta) 3.46 down 0.00031 Table 6B. Down regulated in metastatic cancers versus normal sample set2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction pvalue
 IC_N93i191_at4 N93191 2730 EST 3.25 donwn 0.00232
 rc_N93246_f_at N93246 2731 EST 3.03 down 0.00049
 rc_N93764_at N93764 2737 EST 5.92 down 0.0109
 n94146_at N94146 2739 EST 8.05 down 0
 rc_N94367_a4t n94367 2740 est 8.79 down 0.01003
 rc_N94930_at N94930 2741 multiple PDZ domain protein 10.06 down 0.00226
 rc_N95495_at N95495 2742 EST 5.61 down 0.00308
 rc_N95585_at N95585 2743 EST 3.1 down 0.0083
 N99542_at N99542 2747 orosomucoid 1 8.41 down 0.00001
 rc_N99866_at N99866 2748 EST 3.13 down 0.04148
 rc_R00296_at R00296 2750 EST 3.98 down 0.04632
 rc_R00843_s_at R00843 2741 fragile histidine triad gene 3.68 down 0.03578
 rc_R01023_s_at R01023 2752 glucokinase (heoxkinase 4) regulatory protein 50.71 don 0.00321
 rc_R01081_at R01081 2753 EST 3.3 down 0.00839
 glucose-6-phosphatase, catalytic (glycogen
 rc_R02365_f_at R02365 2755 storage disease type 1, von Gierke disease) 17.17 down 0.00124
 rc_R02371_at R02371 2756 EST 3.57 down 0.00009
 rc_R02572_at R02572 2757 fibronectin 1 7.1 down 0.00059
 rc_R02752_at R02752 2758 EST 3.05 down 0.00362
 rc_R05309_f_at R05309 2759 EST 3.72 down 0.0008
 rc_R05490_at R05490 2761 SEC24 (S. cerevisiae) related gene family, 3.03 down 0.00317
 rc_R05518_at R05518 2762 EST 4.15down 0.0125
 rc_R06002_s_at R06002 2763 EST 10.15 down 0.00003
 rc_R06271_s_at R06271 2766 EST 6.14 down 0.000063
 rc_R06726_s_at R06726 2770 aprotease inhibitor 1 (anti-elastase), alpha-1 12.26 down 0.03905
 rc_R06746_at R06746 2771 EST 15.77 down 0.00009
 rc_R06764_s_at R06764 2772 aplipoprotein Ag(x) antigen) 4.91 down 0.00167
 rc_R06977_f_at R06977 2775 glucokinase (hexolinase 4) regulatory proteine 6.1 down 0.00049
 rc_R07637-at R07637 2778 EST 3.04 down 0.00118
 rc_R08548_at R08548 2779 EST 9.94 down 0.00326
 rc_R08564_at R08564 2780 plasminogen-like 60.18 down 0.00091 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue

rc_R08615_s_at R08615 2781 homogentisate 1,2-dioxygenase (homogentisate 21.85 down 0.00026
 rc_R09053_at R08850 2782 EST 12.55 down 0.00009
 rc_R09053_at R09053 2783 EST 5.9 down 0.0002
 rc_R10138_at R10138 2784 EST 4 down 0.00032
 rc_R10287_at R10287 2785 EST 11.2 down 0.0003
 rc_R10378_s_at R10378 2786 fibrinogen-like 1 8.13 down 0.00189
 rc_R10662_f_at R10662 2787 mutL (E. coli) homolog 1 (colon cancer, 3.2 down 0.0005
 rc_R10684_at R10684 2788 EST 5.51 down 0.00741
 rc_R12472_at R12742 2789 EST 55.18 down 0.00011
 rc_R12579_at R12579 2790 EST 3.5 down 0.00137
 rc_R15825_r_at R15825 2792 KIAA0946 protein; Huntingtin interacting protein 5.33 down 0.00391
 rc_R16098_at R16098 2793 EST 63.41 down 0.00038
 rc_R17762_at R17762 2795 EST 3.37 down 0.01822
 rc_R21232_at R21232 2798 EST 3.56 down 0.00246
 rc_R22196_at R22196 2799 EST 3.75 down 0.02867
 rc_R22905_at R22905 2801 EST 4.64 down 0.0043
 rc_R26904_f_at R26904 2805 EST 3.51 down 0.00058
 R31641_at R31641 2814 EST 9.96 down 0.00011
 rc_R31917_s_at R31917 2815 EST 3.91 down 0.00071
 rc_R32036_s_at R32036 2816 interleukin 1 receptor-like 1 4.02 down 0.00051
 rc_R32440_at R32440 2817 EST 7.41 down 0.00159
 rc_R32490_s_at R32490 2818 EST 8.95 down 0.00215
 rc_R33146_at R33146 2819 EST 7 down 0.00043
 rc_R34133_at R34133 2821 EST 4.13 down 0.00008
 rc_R34362_at R34362 2822 KIAA0327 gene product 5.4 down 0.04615
 rc_R36228_at R36228 2824 EST 4.39 down 0.00033
 rc_R36989_s_at R36989 2826 hypothetical protein, estradiol-induced 13.7 down 0.00056
 rc_R37128_s_at R37128 2827 complement component 4A 39.51 down 0.00364
 rc_R38185_at R38185 2829 EST 6.32 down 0.00063
 rc_R38709_s_at R38709 2833 superoxide dismutase 2, mitochondrial 8.23 down 0.01578
 rc_R39234_r_at R39234 2835 EST 3.24 down 0.0412 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank Seq iD Known Gene Name Fold Change Direction Pvalue
 rc_R40395_s_at R40395 2841 lecithin-cholesterol acyltransferase 37.33 down 0.00032
 rc_R40492_at R40492 2842 EST 8.89 down 0.00229
 rc_R40556_s_at R40556 2843 EST 3.57 down 0.00184
 rc_R40899_f_at R40899 2844 glycine receptor, beta 9.11 down 0.0009
 rc_R40946_f_at R40946 2845 crystallin, zeta (quinone reductase) 6.14 down 0.00156
 rc_R42241_at R42241 2846 EST 3.97 down 0.00129
 rc_R43166_i_at R43166 2847 EST 3.37 down 0.00919
 rc_R43174_s_at R43174 2848 paraoxonase 1 74.04 down 0.00038
 rc_R43365_at R43365 2850 EST 5.37 down 0.00103
 rc_R43799_at R43799 2851 EST 16.35 down 0.00208
 rc_R43910_at R43910 2852 EST 5.71 down 0
 rc_R44025_at R44025 2854 EST 4.4 down 0.01325
 rc_R44761_at R44761 2858 aryl hydrocarbon receptor nuclear translocator 3.12 down 0.02663
 rc_R45656_i_at R45656 2865 EST 10.21 down 0.00179
 rc_R48307_at R48307 2870 EST 7.18 down 0.00007
 rc_R48540_s_at R48540 2873 EST 6.05 down 0.00086
 rc_R48732_s_at R48732 2876 EST 5.12 down 0.00837
 rc_R49035_at R49035 2877 EST 8.02 down 0.00991
 rc_R49459_s_at R49459 2882 transferrin receptor 2 85.61 down 0.00048
 rc_R49602_at R49602 2885 EST 36.5 down 0.00001
 R50008_s_at R50008 2887 7-dehydrocholesterol reductase 6.67 down 0.00409
 rc_R51256_at R51256 2889 EST 3.04 down 0.00286
 rc_R51309_at R51309 2890 KIAA1077 protein 3.54 down 0.04112
 rc_R51831_at R51831 2891 EST 5.03 down 0.00761
 rc_R52800_at R52800 2895 EST 3.96 down 0.00749
 rc_R52822_i_at R52822 2896 EST 12.79 down 0.00001
 rc_R52949_at R52949 2897 EST 3.46 down 0.00395
 rc_R54416_at R54416 2901 EST 3.14 down 0.00236
 rc_R56094_at R56094 2905 EST 4.87 down 0.00214
 rc_R56602_at R56602 2907 Ig superfamily protein 3.06 down 0.02464
 rc_R59221-at R59221 2912 progesterone binding protein 7.54 down 0.00159 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_R59325_at R59325 2914 EST 4.48 down 0.00117
 rc_R59722_at R59722 2916 EST 19.74 down 0.00016
 rc_R61740_f_at R61740 2923 EST 4.02 down 0.00321
 rc_R62173_f_at R62173 2924 UDP-glucose dehydrogenase 5.76 down 0.0006
 rc_R62519_f_at R62519 2926 EST 10.83 down 0.00243
 R63545_at R63545 2927 EST 5.4 down 0.00202
 rc_R64131_at R64131 2930 EST 20.58 down 0.01028
 rc_R64144_s_at R64144 2932 cAMP responsive element

binding protein-like 2 4.58 down 0.00495
 R64199_at R64199 2933 SEC22, vesicle trafficking protein (S. cerevisiae)- 9.19 down 0.00387
 rc_R65593_s_at R65593 2935 kynurenine 3-monooxygenase (kynurenine 3- 21.27 down 0.00007
 R67751_at R67751 2939 EST 3.12 down 0.00319
 rc_R67970_s_at R67970 2940 gamma-glutamyl carboxylase 9.45 down 0.00212
 rc_R69031_at R69031 2941 EST 3.19 down 0.00798
 R69417_at R69417 2942 EST 7.79 down 0.03795
 rc_R70790_at R70790 2948 EST 4.07 down 0.02354
 rc_R71491_at R71491 2954 EST 3.55 down 0.01903
 rc_R73485_at R73485 2958 EST 7.77 down 0.0009
 rc_R73816_at R73816 2961 EST 11.53 down 0.00259
 R77628_at R77628 2966 insulin induced gene 1 29.23 down 0.00122
 R80048_at R80048 2972 EST 12.28 down 0.00128
 R80573_at R80573 2973 EST 3.08 down 0.02126
 rc_R82074_f_at R82074 2974 syndecan 1 6.66 down 0.01336
 R82229_at R82229 2975 phosphatidylserine decarboxylase 3.08 down 0.03455
 rc_R82837_at R82837 2976 KIAA0970 protein 5 down 0.00181
 R87373_s_at R87373 2978 EST 4.09 down 0.02253
 rc_R89811_s_at R89811 2980 HGF activator 62.51 down 0.00148
 rc_R91503_s_at R91503 2982 ATP_binding cassette, sub-family C (CFTR/MRP), 9.64 down 0.00584
 rc_R92458_f_at R92458 2986 hemoglobin, gamma G 3.31 down 0.00763
 rc_R92475_s_at R92475 2987 flavin containing monooxygenase 3 26.13 down 0
 rc_R92737_at R92737 2988 EST 4.53 down 0.04447
 rc_R92768_at R92768 2989 EST 13.2 down 0.00001 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_R93714_at R93714 2992 fetuin B 10.42 down 0.00043
 R93776_s_at R93776 2993 EST 39.32 down 0.00176
 rc_R93908_at R93908 2994 EST 5.8 down 0.02699
 R94662_at R94662 2995 heme-binding protein 4.41 down 0.02301
 rc_R94674_s_at R94674 2996 EST 10.76 down 0.00008
 R96417_at R96417 2998 EST 3.9 down 0.00019
 rc_R96822_at R96822 3000 EST 8.25 down 0.00008
 rc_R97302_at R97302 3003 EST 3.73 down 0.01887
 cytochrome P450, subfamily VIIIB (sterol 12
 rc_R97419_at R97419 3004 alpha_hydroxylase), polypeptide 1 65.07 down 0.0039
 rc_R97711_at R97711 3005 EST 3.37 down 0.00838
 rc_R97798_at R97798 3007 EST 3.79 down 0.00015
 R98073_at R98073 3009 EST 46.87 down 0
 rc_R98074_at R98074 3010 EST 9.21 down 0.00048
 rc_R98413_at R98413 3012 EST 9.71 down 0.00007
 rc_R98624_at R98624 3013 EST 21.32 down 0
 rc_R98774_at R98774 3014 EST 3.93 down 0.00001
 rc_R99591_at R99591 3016 CD5 antigen-like (scavenger receptor cysteine 9.52 down 0.00006
 rc_R99909_at R99909 3017 EST 4.27 down 0.00045
 S48983_at S48983 3018 serum amyloid A4, constitutive 23.04 down 0.00022
 S52028_s_at S52028 3019 cystathionase (cystathionine gamma-lyase) 3.21 down 0.00476
 S62539_s_at S62539 3022 insulin receptor substrate 1 3.7 down 0.01307
 S67325_at S67325 3024 propionyl Coenzyme A carboxylase, beta 4.19 down 0.00151
 aldo-keto reductase family 1, member C4
 (chlordecone reductase; 3-alpha hydroxysteroid
 S68287_at S68287 3025 dehydrogenase, type I; dihydrodiol 24.11 down 0
 S68805_at S68805 3026 glycine amidinotransferase (L-arginine:glycine 18.19 down 0.00083
 S69232_at S69232 3027 electron-transferring-flavoprotein dehydrogenase 4.9 down 0.00017
 S70004_at S70004 3029 glycogen synthase 2 (liver) 9.96 down 0.00001
 S72370_at S72370 3030 pyruvate carboxylase 5.31 down 0.00075
 S72370_at S72370 3030 pyruvate carboxylase 4.54 down 0.0001 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 S74728_at S74728 3033 antiquitin 1 5.01 down 0.00008
 S77356_at S77356 3034 EST 5.83 down 0.00122
 S77410_at S77410 3035 angiotensin receptor 1 10.4 down 0
 S90469_at S90469 3040 P450 (cytochrome) oxidoreductase 4.32 down 0.0182
 S95936_at S95936 3041 transferrin 19.76 down 0.02009
 rc_T03441_f_at T03441 3044 cytochrome b-561 5.74 down 0.02781
 rc_T03651_s_at T03651 3047 tubulin, beta polypeptide 6.47 down 0.00843
 T08879_at T08879 3049 cathepsin F 5.29 down 0.0008
 rc_T10108_s_at T10108 3050 EST 3.85 down 0.01155
 rc_t10264_s_at T10264 3051 EST 3.84 down 0.00874
 rc_T10322_at T10322 3053 dihydropyrimidinase-like 2 4.23 down 0.01527
 rc_T10822_at T10822 3055 EST 3.16 down 0.00635
 rc_T15482_f_at T15482 3060 EST 5.04 down 0.00233
 rc_T15674_f_at T15674 3061 EST 4.12 down 0.02111
 rc_T16175_s_at

T16175 3064 protein tyrosine phosphatase, non-receptor type 3.07 down 0.01007
 rc_T16269_at
 T16269 3067 EST 3.36 down 0.00282
 rc_T16478_at T16478 3070 EST 4 down 0.01041

 rc_T16484_s_at T16484 3071 EST 7.69 down 0.00805
 rc_T17411_s_at T17411 3078
 transthyretin (prealbumin, amyloidosis type I) 13.49 down 0.00203
 rc_T23430_at T23430 3080
 EST 3.12 down 0.00949
 rc_T23680_at T23680 3084 calcium channel, voltage-dependent,
 gamma 3.29 down 0.0003
 rc_T23882_s_at T23882 3085 kininogen 42.85 down 0.00641

 rc_T23986_s_at T23986 3086 hydroxyacyl glutathione hydrolase; glyoxylase 2 7.26 down 0.0062

 rc_T24055_s_at T24055 3087 ribosomal protein L26 3.9 down 0.00046
 rc_T24106_at T24106
 3089 EST 12.13 down 0.01687
 rc_T25506_at T25506 3090 EST 4.51 down 0.00529

 T30341_s_at T30341 3101 EST 3.04 down 0.04567
 rc_T33011_at T33011 3104 EST 3.57 down
 0.02486
 T39897_s_at T39897 3114 androgen induced protein 10 down 0.00466

 rc_T40936_at T40936 3118 EST 46.92 down 0.00056
 rc_T40995_f_at T40995 3119 alcohol
 dehydrogenase 3 (class I), gamma 13.25 down 0.01531 Table 6B. Down regulated in metastatic cancers
 versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change
 Direction Pvalue
 rc_T41047_s_at T41047 3120 EST 4.74 down 0.00015
 rc_T41232_at
 T41232 3122 EST 3.57 down 0.00846
 rc_T46901_at T46901 3123 EST 77.28 down 0.0006

 rc_T47778_s_at T47778 3127 fibrinogen, A alpha polypeptide 30 down 0.01401
 rc_T48039_s_at
 T48039 3129 protein C (inactivator of coagulation factor Va 84.39 down 0.00112

 rc_T48075_f_at T48075 3130 hemoglobin, alpha 1 32.56 down 0.00172
 rc_T48278_at T48278
 3132 EST 15.02 down 0.04751
 rc_T48980_s_at T48980 3134 calmodulin 1 (phosphorylase
 kinase, delta) 4.2 down 0.0046
 rc_T49061_at T49061 3135 EST 3.06 down 0.00768

 rc_T51150_at T51150 3137 EST 10.52 down 0.00377
 solute carrier family 22
 (extraneuronal
 rc_T51617_at T51617 3138 monoamine transporter), member 3 17.67 down
 0.00018
 rc_T51930_at T51930 3139 EST 9.99 down 0.00066
 rc_T52564_at T52564 3141
 EST 3.28 down 0.01506
 rc_T52813_s_at T52813 3142 putative lymphocyte G0/G1 switch gene
 16.71 down 0.03897
 rc_T54160_s_at T54160 3145 EST 3.24 down 0.00168
 rc_T55547_at
 T55547 3148 EST 3.28 down 0.00047
 rc_T56264_s_at T56264 3149 apolipoprotein C-II 53.04
 down 0.00938
 rc_T56278_s_at T56279 3150 H factor (complement)-like 3 28.39 down
 0.00016
 rc_T56281_f_at T56281 3151 RNA helicase-related protein 32.34 down 0.00002

 T57140_s_at T57140 3152 paraoxonase 3 28.8 down 0
 rc_T58032_s_at T58032 3153 3-
 hydroxyanthranilate 3,4-dioxygenase 8.86 down 0.00023
 rc_T58756_at T58756 3156 EST 13.39
 down 0.00013
 rc_T58775_at T58775 3157 small inducible cytokine subfamily A (Cys-Cys),
 21.18 down 0.00006
 rc_T59148_s_at T59148 3158 carbamoyl-phosphate synthetase 1,
 mitochondrial 88.889 down 0
 rc_T60407_at T60407 3161 EST 6.6 down 0.00167

 rc_T61256_s_at T61256 3162 ketohexokinase (fructokinase) 13.59 down 0.00425
 vitronectin
 (serum spreading factor, somatomedin
 rc_T61373_s_at T61373 3163 B, complement S-protein)
 44.9 down 0.03172
 rc_T61389_f_at T61389 3164 haptoglobin 18.95 down 0.04873

 rc_T61649_f_at T61649 3165 superoxide dismutase 2, mitochondrial 26.09 down 0.00734 Table 6B.
 Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank Seq ID
 Known Gene Name Fold Change Direction Pvalue
 rc_T61801_s_at T61801 3167 hemopexin 25.7
 down 0.01362
 rc_T63364_at T63364 3170 ficolin (collagen/fibrinogen domain-containing) 3 6.72
 down 0.00383
 rc_T63490_at T63490 3171 EST 16.54 down 0
 rc_T64575_s_at T64575
 3172 EST 10.46 down 0.00014
 rc_T64887_f_at T64887 3173 protein phosphatase 5, catalytic
 subunit 5.66 down 0.00349
 rc_T65972_at T65972 3177 EST 3.21 down 0.04847

 rc_T66189_s_at T66189 3178 glutaryl-Coenzyme A dehydrogenase 8.61 down 0.00003
 succinate
 dehydrogenase complex, subunit D,
 T67231_at T67231 3181 integral membrane protein 7.04
 down 0.03554
 rc_T67705_s_at T67705 3183 asialoglycoprotein receptor 2 31.6 down
 0.00705
 rc_T67931_at T67931 3184 fibrinogen, B beta polypeptide 49.55 down 0

 T68083_at T68083 3185 short-chain dehydrogenase/reductase 1 4.03 down 0.01593

 rc_T68426_s_at T68426 3186 CD81 antigen (target of antiproliferative antibody 3.11 down
 0.01634
 T68510_at T68510 3187 EST 3.87 down 0.00617
 rc_T68711_at T68711 3188 EST

37.65 down 0.00036
 rc_T68855_at T68855 3189 EST 34.04 down 0
 rc_T68873_f_at T68873 3190 metallothionein 1L 28.72 down 0.02953
 rc_T68878_f_at T68878 3191 carboxylesterase 1 (monocyte/macrophage 60.35 down 0.00409
 rc_T69009_s_at T69009 3192 quinoid dihydropteridine reductase 6.54 down 0.00145
 rc_T69020_at T69020 3193 EST 5.39 down 0.00383
 rc_T69029_f_at T69029 3194 haptoglobin 33.18 down 0.02825
 rc_T69164_at T69164 3195 EST 4.38 down 0.00548
 rc_T69284_s_at T69284 3196 mannose-binding lectin (protein C) 2, soluble 36.53 down 0
 T69384_at T69384 3198 period (Drosophila) homolog 1 5.88 down 0.01219
 rc_T69728_at T69728 3199 heat shock 90kD protein 1, beta 3.98 down 0.00786
 rc_T70087_at T70087 3200 EST 4.7 down 0.00173
 rc_T71012_s_at T71012 3201 fibrinogen, B beta polypeptide 43.61 down 0.00743
 rc_T71021_at T71021 3202 EST 6.74 down 0.0017
 rc_T71373_at T71373 3203 EST 83.08 down 0.00069
 rc_T71776_at T71776 3204 EST 10.3 down 0.00897
 rc_T71978_at T71978 3205 EST 4.39 down 0.0017 Table 6B.

Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_T72171_s_at T72171 3206 thyroxine-binding globulin 10.41 down 0.00163
 rc_T72268_s_at T72268 3207 B-factor, properdin 7.43 down 0.01197
 rc_T72502_at T72502 3208 EST 8.87 down 0.00009
 rc_T72629_i_at T72629 3209 EST 3.24 down 0.00556
 rc_T72906_at T72906 3210 EST 7.56 down 0.00062
 rc_T73420_at T73420 3211 short-chain dehydrogenase/reductase 1 4.58 down 0.00656
 rc_T73433_s_at T73433 3212 angiotensinogen 48.3 down 0.00049
 rc_T73442_at T73442 3213 EST 94.41 down 0
 alanine-glyoxylate aminotransferase (oxalosis I);
 rc_T73739_s_at T73739 3214 hyperoxaluria I; glycolicaciduria; serine-pyruvate 16.18 down 0.00277
 rc_T74542_s_at T74542 3215 UDP glycosyltransferase 2 family, polypeptide 32.36 down 0.00004
 rc_T74608_at T74608 3216 hydroxyacid oxidase (glycolate oxidase) 1 14.03 down 0
 rc_T74884_r_at T74884 3217 EST 3.76 down 0.02547
 rc_T77729_f_at T77729 3218 pyruvate carboxylase 7.29 down 0.00022
 rc_T78433_s_at T78433 3220 glycogen synthase 2 (liver) 8.62 down 0.00072
 rc_T78889_s_at T78889 3221 fibronectin 1 19.87 down 0.00912
 rc_T79758_at T79758 3224 EST 3.94 down 0.00581
 rc_T79842_at T79842 3225 EST 3.16 down 0.03159
 rc_T79863_at T79863 3226 EST 5.62 down 0.00074
 rc_T81315_at T81315 3227 EST 4.28 down 0.00187
 rc_T82254_at T82254 3229 EST 3.82 down 0.00091
 rc_T82259_at T82259 3230 EST 3.12 down 0.01122
 rc_T82323_at T82323 3231 immunoglobulin superfamily, member 4 10.14 down 0
 rc_T83356_s_at T83356 3232 apolipoprotein H (beta-2-glycoprotein I) 64.34 down 0.00802
 T83397_at T83397 3233 phytanoyl-CoA hydroxylase (Refsum disease) 63.6 down 0
 T85532_f_at T85532 3236 EST 4.33 down 0.00591
 rc_T86464_at T86464 3237 EST 3.17 down 0.00498
 rc_T86482_at T86482 3238 transferrin 11.15 down 0.00006
 rc_T86978_s_at T86978 3239 glutamate dehydrogenase 1 9.44 down 0.00006
 rc_T87174_at T87174 3240 EST 21.71 down 0.00681
 rc_T90037_at T90037 3246 EST 3.99 down 0.0016 Table 6B.

Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_T90492_at T90492 3248 EST 3.88 down 0.00454
 rc_T90520_at T9052 3249 EST 8.67 down 0.00072
 rc_T90531_at T90531 3250 EST 3.6 down 0.00301
 rc_T90841_f_at T90841 3251 EST 5.74 down 0.01876
 rc_T91161_at T91161 3253 EST 3.48 down 0.00002
 rc_T91348_at T91348 3254 EST 3.57 down 0.00011
 rc_T92950_at T92950 3256 EST 3.01 down 0.00497
 rc_T94862_at T94862 3258 EST 3.07 down 0.01417
 rc_T95064_at T95064 3260 EST 5.75 down 0.00604
 rc_T95515_s_at T95515 3261 KIAA0249 gene product 6.77 down 0.0001
 T95813_f_at T95813 3262 KIAA1051 protein 38.38 down 0.00008
 rc_T96969_at T96969 3264 EST 3.42 down 0.00053
 rc_T97234_at T97234 3265 EST 4.34 down 0.00263
 rc_T98199_i_at T98199 3267 EST 4.86 down 0.00431
 rc_T98676_at T98676 3269 EST 46.94 down 0.0001
 rc_T99636_s_at T99636 3271 complement component 3 29.6 down 0.00051
 U00115_at U00115 3272 B-cell CLL/lymphoma 6 (zinc finger protein 51) 5.18 down 0.00045
 glucose-6-phosphatase, catalytic (glycogen
 U01120_at U01120 3274 storage disease type I, von Gierke disease) 13.41 down 0.00147
 solute carrier family 1 (glial high affinity glutamate

U01824_at U01824 3276 transporter), member 2 3.2 down 0.00021
 U02020_at U02020 3277 pre-B-cell colony-enhancing factor 3.37 down 0.01112
 U02388_at U02388 3278 cytochrome P450, subfamily IVF, polypeptide 2 9.38 down 0.00001
 U03056_at U03056 3280 hyaluronoglucosaminidase 1 6.64 down 0
 U03105_at U03105 3281 proline-rich protein with nuclear targeting signal 4.69 down 0.00017
 ald-keto reductase family 1, member C1
 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-
 U05861_at U05861 3285 ydroxysteroid dehydrogenase) 23.22 down 0.00002
 U06641_s_at U06641 3287 UDP glycosyltrasferse 2 family, polypeptide 24.32 down 0.00001
 U06863_at U06863 3288 follistatin-like 1 3.09 down 0.000091
 U08006_s_at U08006 3290 complement component 8, alpha polypeptide 16 down 0.00111 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 U08198_rna1_at U08198 3292 complement component 8, gamma polypeptide 19.71 down 0
 U08854_s_at U08854 3293 UDP glycosyltransferase 2 family, polypeptide 7.38 down 0.00005
 U11313_at U11313 3297 sterol carrier protein 2 5.44 down 0.00187
 U12778_at U12778 3301 acyl-Coenzyme A dehydrogenase, 5.68 down 0.00116
 sulfotransferase family 2A,
 U13061_rna1_at U13061 3302 dehydroepiandrosterone (DHEA) -preferring, 11.32 down 0.00048
 U16660_at U16660 3313 enoyl Coenzyme A hydratase 1, peroxisomal 3.96 down 0.00002
 U19495_s_at U19495 3319 stromal cell-derived factor 1 4.59 down 0.00011
 U19523_at U19523 3320 GTP cyclohydrolase 1 (dopa-responsive 5.25down 0.00029
 U20530_at U20530 3322 secreted phosphoprotein 2, 24kD 16.93 down 0
 U20938_at U20938 3324 dihydropyrimidine dehydrogenase 3.92 down 0.00053
 U21931_at U21931 3326 fructose-bisphosphatase 1 3.4 down 0.00709
 cytochrome P450, subfamily IIA (phenobarbital-
 U22029_f_at U22029 3327 inducible), polypeptide 7 71.98 down 0
 U22961_s_at U22961 3330 albumin 22.22 down 0.01531
 aldehyde dehydrogenase 4 (glutamate gamma-
 U24266_at U24266 3331 semialdehyde dehydrogenase; pyrroline-5- 14.54 down 0
 U25182_at U25182 3333 trioredoxin peroxidase (antioxidant enzyme) 3.13 down 0.02543
 U26173_s_at U26173 3335 nuclear factor, interleukin 3 regulated 6.4 down 0.00001
 U27460_at U27460 3339 UDP-glucose pyrophosphorylase 2 11.46 down 0.00088
 solute carrier family 6 (neurotransmitter
 U27699_at U27699 3340 transporter, betaine/GABA), member 12 3.65 down 0.00381
 U28838_at U28833 3341 Down syndrome candidate region 1 3.3 down 0.00306
 U29953_rna1_at U29953 3342 pigment epithelium-derived factor 15.33 down 0.00212
 U31449_at U31449 3345 transmembrane 4 superfamily member 4 11.53 down 0.00187
 U32576_rn1_at U32576 3347 apolipoprotein C-IV 18.59 down 0.00005
 U32576_rn1_at U32576 3347 apolipoprotein C-IV 5.81 down 0.04343
 U32989_at U32989 3348 tryptophan 2,3-dioxygenase 10.07 down 0.02825
 aldehyde dehydrogenase 9 (gamma-
 U34252_at U34252 3350 aminobutyraldehyde dehydrogenase, E3 4.31 down 0.00613
 U36922_at U36922 3352 EST 3.06 down 0.01388 Table 6B. Down regulated in metastatic canvers versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 macrophage stimulating 1 (hepatocyte growth
 U3055_ma1_s_at U37055 3353 factor-like), macrophages stimulating, pseudogene 18.28 down 0
 U44111_at U44111 3363 histamine N-methyltransferase 3.5 down 0.00942
 U46499_at U46499 3365 microsomal glutathione S-transferase 1 4.27 down 0.00244
 U46689_at U46689 3366 aldehyde dehydrogenase 10 (fatty aldehyde 3.5 down 0.01292
 U48296_at U48296 3369 protein tyrosine phosphatase type IVA, member 1 4.25 down 0.02037
 U48707_at U48707 3371 protein phosphatase 1, regulatory (inhibitor) 14.22 down 0
 U48959_at U48959 3372 myosin, light polypeptide kinase 3.61 down 0.00084
 U49082_at U49082 3373 transporter protein 9.17 down 0.00088
 U49248_at U49248 3374 ATP-binding cassette, sub-family C (CFTR/MRP), 7.06 down 0.00067
 U49352_at U49352 3375 2,4-dienoyl CoA reductase 1, mitochondrial 5.41 down 0.02371
 U49785_at U49785 3376 D-dopachrome tautomerase 3.84 down 0.00044
 U50196_at U50196 3377 adenosine kinase 3.82 down 0.1425
 U50527_s_at U50527 3378 EST 3.93 down 0.00123
 U50929_at U50929 93380 betaine-homocysteine methyltransferase 36.91 down 0
 Ut1010_s_at U51010 3381 nicotinamide N-methyltransferase 27.79 down 0.00366
 U51333_s_at U51333 3383 hexokinase 3

(white cell) 4.88 down 0.00055
 U51903_at U51903 3387 IQ motif containing GTPase activating protein 2 3.23 down 0.00242
 U53003_at U53003 3388 ES1 (zebrafish) protein, human homolog of 4.84 down 0.00077
 U56814_at U56814 3393 deoxyribonuclease I-like 3 29.43 down 0.00003
 U56814_at U56814 3393 deoxyribonuclease I-like 3 11.36 down 0.00001
 U57721_at U57721 3395 kynureninase (L-kynurenine hydrolase) 4.34 down 0.0197
 U60205_at U60205 3401 sterol-C4-methyl oxidase-like 5.16 down 0.00061
 U62389_at U62389 3402 isocitrate dehydrogenase 1 (NADP+), soluble 3.15 down 0.03949
 U66674_at U66674 3408 ATP-binding cassette, sub-family C (CFTR/MRP), 6.13 down 0.00127
 U67963_at U67963 3410 lysophospholipase-like 3.19 down 0.00029
 U68233_at U68233 3412 nuclear receptor subfamily 1, group H, member 4 6.76 down 0.00022
 U68494_at U68494 3413 EST 4.82 down 0.00881
 U69141_at U69141 3414 glutaryl-Coenzyme A dehydrogenase 3.06 down 0.00053
 U70732_mal_at U70732 3415 glutamic-pyruvate transaminase (alanine 27.63 down 0
 U70732_mal_at U70732 3415 glutamic-pyruvate transaminase (alaine 5.64 down 0.00146 Table 6B, Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 U73514_at U73514 3419 hydroxyacyl-Coenzyme A dehydrogenase, type II 3.79 down 0.01392
 U73682_at U73682 3420 meningioma expressed antigen 6 (coiled-coil 3.08 down 0.01249
 U76376_at U76376 3425 karakiri, BCL2-interacting protein (contains only 11.77 down 0.00002
 U77396_at U77396 3426 LPS_induced TNF-alpha factor 4.47 down 0.00108
 U77594_at U77594 3428 retinoic acid receptor responder (tazarotene 11.95 down 0.00527
 U78190_mal_at U78190 3431 GTP cyclohydrolase 1 feedback regulator protein 3.94 down 0.034
 U79294_at U79294 3435 Phosphatidic acid phosphatase type 2b 3.13 down 0.00129
 U79303_at U79303 3436 protein predicted by clone 23882 4.45 down 0
 U79716_at U79716 3437 reelin 3.51 down 0.00053
 solute carrier family 9 (sodium/hydrogen
 U82108_s_at U82108 3441 exchanger), isoform 3 regulatory factor 2 3.19 down 0.01545
 U82468_at U82468 3442 tubby like protein 1 3.34 down 0.0097
 U84569_at U84569 3445 chromosome 21 open reading frame 2 3.46 down 0.01844
 U86529_at U86529 3451 glutathione S-transferase zeta 1 3.41 down 0.0118
 U90544_at U90544 3454 solute carrier family 17 (sodium phosphate), 6.42 down 0.00023
 U90545_at U90545 3455 solute carrier family 17 (sodium phosphate), 4.14 down 0.00005
 U95090_at U95090 3464 nephrosis 1, congenital, Finnish type (nephrin) 14.01 down 0.00018
 U95090_at U95090 3464 nephrosis 1, congenital, Finnish type (nephrin) 7.44 down 0.00004
 W03796_at W03796 3468 EST 8.3 down 0.0032
 W07723_at W07723 3471 EST 3.51 down 0.00026
 rc_W15528_at W15528 3475 EST 3.56 down 0.00424
 W20094_at W20094 3477 DKFZP586A0522 protein 38.09 down 0.00188
 W20276_f_at W20276 3478 EST 3.82 down 0.00033
 rc_W20467_f_at W20467 3480 EST 7.76 down 0.00008
 W26769_at W26769 3483 CGI-86 protein 8.14 DOWN 0.00204
 W26996_AT W26996 3484 EST 6.42 down 0.00005
 W27023_at W27023 3485 neuroendocrine-specific protein C like (foocen) 6.79 down 0.00805
 W28798_at W28798 3492 phosphodiesterase 6A, cGMP-specific, rod, alpha 7.01 down 0.00017
 W28824_at W28824 3493 EST 15.8 down 0.00006
 W28944_at W28944 3494 EST 37.07 down 0.00205
 rc_W31478_s_at W31478 3496 EST 3.36 down 0.01511 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_W33167_at W22167 3499 EST 8.01 down 0.00026
 W35309_at W35309 3500 EST 3.11 down 0.029
 W36290_s_at W36290 3501 Kreisler (mouse) maf-related leucine zipper 3.94 down 0.02718
 rc_W37382_at W37382 3502 EST 4.37 down 0.00677
 rc_W38407_at W38407 3506 EST 4.17 down 0.00392
 rc_W42483_at W42483 3510 EST 3.04 down 0.02518
 rc_W42789_at W42789 3515 EST 9.38 down 0.00059
 rc_W42996_at W42996 3517 EST 6.18 down 0.00587
 rc_W44745_at W44745 3520 EST 9.02 down 0.00276
 rc_W45051_at W45051 3521 EST 4.68 down 0.00433
 W45259_at W45259 3522 EST 3.78 down 0.0069
 rc_W45560_at W45560 3525 EST 5.06 down 0.00996
 rc_w46391_at W46391 3527 alpha integrin binding protein 63 4.03 down 0.01363
 rc_W46404_at W46404 3528 EST 3.73 down 0.00116
 rc_W47175_at W47175 3534 3-prime-phosphoadenosine 5-prime- 5.54 down

0.00914
 rc_W51951_s_at W51951 3542 dCMP deaminase
 CD36 antigen (collagen) type I receptor,
 W52581_at W52581 3543 thrombospondin receptor)-linke 2 (lysosomal 3.08 down 0.00091
 W52821_at W52821 3544 leucine aminopeptidase 4.02 down 0.03787
 W55903_at W55903 3546 adipose differentiation-related protein; adipophilin 9.12 down 0.00459
 rc_W57821_at W57821 3548 EST 5.03 down 0.00277
 W58540_AT W58540 3553 KIAA1131 protein 4.28 down 0.0184
 rc_W58756_at W58756 3554 EST 17.17 down 0.00087
 rc_W60002_s_at W60002 3555 plastin 3 (T isoform) 4.88 down 0.01694
 rc_W60186_at W60186 3557 EST 3.24 down 0.00228
 rc_W61000_at W61000 3560 EST 3.15 down 0.03143
 rc_W61319_at W61319 3561 EST 3.02 down 0.00031
 W61377_at W61377 356 EST 9.33 down 0.0012
 rc_W61378_s_at W61378 3563 EST 8.31 down 0
 rc_W63728_at W63728 3565 EST 5.03 down 0.00311
 rc_r63785_at W63785 3567 EST 3.91 down 0.04089 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_W67147_at W67147 3568 deleted in liver cancer 1 9.74 down 0.0002
 rc_W67199_at W67199 3569 EST 3.09 down 0.01528
 rc_W67564_s_at @67564 3571 nuclear receptor subfamily, group B, member2 30.34 down 0
 rc_W68721_f_at W68721 3572 cleft lip and palate associated transmembrane 6.34 own 0.01504
 rc_W69675_at W69675 3575 EST 4.42 down 0.00019
 rc_W70115_s_at W70115 3576 histidine ammonia-lyase 1165 down 0.0003
 rc_w70313_at W70313 3578 EST 3 down 0.00643
 rc_W72044_at W72044 3580 insulin induced gene 1 24.58 down 0.00001
 rc_W72079_at W72079 3581 EST 6.36 down 0.00641
 rc_W72972_at W72972 3587 EST 5.61 down 0.00939
 rc_W73194_at W73194 3590 dermatopontin 3.45 Down 0.02211
 rc_W73601_at W73601 3592 EST 32.25 down 0
 rc_W73818_at W73818 3593 EST 4.32 down 0.00385
 rc_W73889_s_at W73889 3594 tetranectin (plasminogen-binding protein 7.46 down 0.00091
 W74158_at W74158 3596 EST 4.81 down 0.00091
 W79046_at @79046 3602 peroxisomal D3,D2-enoyl-CoA isomerase 27.9 down 0.00023
 rc_W79422_s_at W79422 3604 fumarylacetoacetate 14.92 down 0.00059
 rc_W80609_at W80609 3606 EST 4.68 down 0.01729
 W81053_at W81053 3610 EST 4.91 down 0.00164
 rc_W81079_at W81079 3611 EST 3.31 down 0.0167
 protein kinase, interferon-inducible double
 W81268_at W81268 3612 stranded RNA depdnt 4.2 down 0.00007
 rc_W85765_at W85765 3616 EST 3.83 down 0.00379
 rc_W85847_at W85847 3619 EST 7.28 down 0.00024
 rc_W85886_at W85886 3621 EST 3.46 down 0.00814
 rc_W85888_at W85888 3622 EST 3.99 down 0.00697
 rc_W86075_at W86075 3624 est 13.83 down 0.00697
 rc_W86375_s_at W86375 3626 EST 19.29 down 0.0061
 rc_W86431_s_at W86431 3627 protein C inhyibitor (plasminogen activgator inhibitor 14.94 down 0.00152
 rc_W86600_at W86600 3628 EST 32.14 down 0
 rc_W86756_at W86756 3630 retinoid receptor, alpha 3.77 down 0.2472 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 solute carrier family 25 (mitochondrial carrier;
 rc_W86850_f_at W86850 3631 citrate trnsporter), ember 1 4.9 down 0.03105
 rc_W87454_at W87454 3632 homogentisate 1,2-dioxygenase (homogentisate 7.93 down 0.00149
 rc_W87480_at W87480 3633 STAT induced STAT inhibitor-2 3.24 down 0.01063
 rc_w87532_at W87532 3634 putative glycine-N-acyltransferase 12.34 down 0.00014
 rc_W87606_s_at W87606 3635 protein Z, vitamin K-dependent plasma 9.23 down 0.00085
 rc_W8778_at W87781 3636 EST 6.1 down 0.00045
 rc_w87824_at W87824 3637 EST 3.67 down 0.01559
 rc_W8568_at W88568 3638 glycogenin 2 4.16 down 0.00111
 rc_W88946_at W88946 3639 putative glycine-N-acyltransferase 58.26 down 0
 rc_W88985_at W88985 3640 KIAA0903 protein 3.94 down 0.00295
 rc_W89178_at W89178 3641 transferrin receptor 2 10.85 down 0.00116
 rc_W90128_s_at W90128 3643 X-box binding protein 1 10.04 down 0.00018
 rc_W90455_s_at W90455 3646 alpha-2-macroglobulin 10.35 down 0.00063
 rc_W90560_at W90560 3647 EST 3.35 down 0.00388
 rc_W90583_r_at W90583 3648 EST 3.435 down 0.00318
 rc_W90766_at W90766 3649 EST 7.58 DOWN 0.00057
 rc_W92148_s_at W92148 3650 kininogen 51.09 down 0.00376
 rc_W92713_at W92713 3654 EST 16.55 down 0.00097
 rc_W92771_s_at W92771 3655 glycine cleavage system protein H (aminomethyl 4.36

down 0.0064
 rc_W94427_at W94427 3659 EST 3.86 down 0.02649
 rc_W94942_i_at W94942 3661 dual specificity phosphatase 10 7.23 down 0.00137
 rc_W95041_at W95041 3662 EST 12.79 down 0.00001
 W95795_at W95795 3665 EST 7.8 down 0.00359
 X00129_at X00129 367 retinol-binding protein 4, interstitial 18.57 down 0.02378
 AFFX-HSAC07/X00351_M_st X00351 3668 actin, beta 4.76 down 0.0003
 X01038_mal_s_at X01038 3669 apolipoprotein A-I, apolipoprotein C-III 19.97 down 0.0275
 X01388_at X01388 3670 apolipoprotein C-III 10.9 down 0.01246
 X02160_at X02160 3671 insulin receptor 5.29 down 0.0001
 X02160_at X02160 3671 insulin receptor 3.27 down 0.0007
 X02176_s_at X02176 3672 complement component 9 9.61 down 0.00004 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 X02750_at X02750 3673 protein C (inactivator of coagulation factors Va 7.04 down 0.00079
 vitronectin (serum spreading factor, somatomedin
 X03168_at X03168 3674 B, complement S-protein) 25.88 down 0.00911
 X03350_at X03350 3676 alcohol dehydrogenase 2 (class I), beta 19.32 down 0.00001
 X04085_mal_at X04085 3678 catalase 11.27 down 0.0002
 gap junction protein, beta 1, 32kD (connexin 32,
 X04325_at X04325 3679 Charcot-Marie-Tooth neuropathy, X-linked) 10.17 down 0.00061
 X04729_s_at X04729 3682 plasminogen activator inhibitor, type I 3.15 down 0.01337
 guanine nucleotide binding protein (G protein),
 X04828_at X04828 3683 alpha inhibiting activity polypeptide 2 5.22 down 0.01278
 X05409_at X05409 3684 aldehyde dehydrogenase 2, mitochondrial 3.99 down 0.01029
 X06562_at X06562 3686 growth hormone receptor 10.87 down 0.00001
 X07173_at X07173 3690 inter-alpha (globulin) inhibitor, H2 polypeptide 30.3 down 0.00016
 cytochrome P450, subfamily IID (debrisoquine,
 X07618_s_at X07618 3691 sparteine, etc., -metabolising), polypeptide 7a 35.79 down 0.00065
 cytochrome P450, subfamily IID (debrisoquine,
 X07618_s_at X07618 3691 sparteine, etc., -metabolising), polypeptide 7a 13.58 down 0
 cytochrome P450, subfamily IID (debrisoquine,
 X07619_s_at X07619 3692 sparteine, etc., -metabolising), polypeptide 7a 4.96 down 0.00004
 X07732_at X07732 3693 hepsin (transmembrane protease, serine 1) 28.21 down 0
 X07767_at X07767 3694 protein kinase, cAMP-dependent, catalytic, alpha 5.94 down 0.00028
 X12662_mal_at X12662 3697 arginase, liver 20.59 down 0
 X13227_at X13227 3698 D-amino-acid oxidase 4.81 down 0.0002
 X13334_at X13334 3699 CD14 antigen 12.77 down 0.00887
 cytochrome P450, subfamily IIA (phenobarbital-
 X13930_f_at X13930 3700 inducible), polypeptide 6 38.52 down 0
 X14690_s_at X14690 3703 pre-alpha (globulin) inhibitor, H3 polypeptide 16.07 down 0.00438
 X14787_at X14787 3704 thrombospondin 1
 acetyl-Coenzyme A acyltransferase 1
 X14813_at X14813 3705 (peroxisomal 3-oxoacyl-Coenzyme A thiolase) 11.61 down 0.0002
 X15422_at X15422 3708 mannose-binding lectin (protein C) 2, soluble 8.29 down 0.00015 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 X16260_s_at X16260 3710 inter-alpha (globulin) inhibitor, H1 polypeptide 44.65 down 0.00933
 X16260_s_at X16260 3710 inter-alpha (globulin) inhibitor, H1 polypeptide 26.39 down 0.0004
 X16349-s_at X16349 3712 sex hormone-binding globulin 9.34 down 0.00007
 X17025_at X17025 3715 isopentenyl-diphosphate delta isomerase 3.13 down 0.0043
 paired basic amino acid cleaving enzyme (furin,
 X17094_at X17094 3717 membrane associated receptor protein) 8.5 down 0
 X52150_mal_s_at X52150 3722 arylsulfatase A 3.51 down 0.00113
 X52520_at X52520 3723 tyrosine aminotransferase 13.51 down 0.00002
 X52541_at X52541 3724 early growth response 1 3.77 down 0.00894
 alanine-glyoxylate aminotransferase (oxalosis I;
 X53414_at X53414 3728 hyperoxaluria I; glycolicaciduria; serine-pyruvate 13.87 down 0.00003
 X53595_s_at X53595 3729 apolipoprotein H (beta-2-glycoprotein I) 27.28 down 0.0066
 X54380_at X54380 3730 pregnancy-zone protein 8.44 down 0.00059
 X55283_mal_s_at X55283 3734 asialoglycoprotein receptor 2 84.99 down 0.00084
 X56411_mal_at X56411 3737 alcohol dehydrogenase 4 (class II), pi polypeptide 25.14 down 0.00144
 X56692_at X56692 3739 C-reactive protein, pentraxin-related 15.15 down 0.01884
 X57025_at X57025 3742 insulin-like growth factor 1 (somatomedin C) 4.72 down 0.00087
 X58022_at X58022 3747 corticotropin

releasing hormone-binding protein 4.09 down 0.00076
 X58528_s_at X58528 3748 ATP-binding cassette, sub-family D (ALD), 4.91 down 0.00728
 X59766_at X59766 3749 alpha-2-glycoprotein 1, zinc 12.96 down 0.0004
 cytochrome P450, subfamily XXVIIA (steroid 27-
 X59812_at X59812 3750 hydroxylase, cerebrotendinous xanthomatosis), 4.65 down 0.036
 X59834_at X59834 3751 glutamate-ammonia ligase (glutamine synthase) 4.29 down 0.00255
 X60673_s_at X60673 3752 adenylate kinase 3 8.3 down 0.00016
 X61123_at X61123 3753 B-cell translocation gene, 1 anti-proliferative 3.2 down 0.00796
 X62822_at X62822 3758 sialyltransferase 1 (beta-galactoside alpha-2,6- 4.89 down 0.00274
 X63359_at X63359 3759 UDP glycosyltransferase 2 family, polypeptide 13.66 down 0.00051
 X64877_at X64877 3766 H factor (complement)-like 3 14.6 down 0
 X64877_s_at X64877 3766 H factor (complement)-like 3 12.33 down 0
 X65727_cds_s_at X65727 3768 glutathione S-transferase A2, glutathione S- 73.64 down 0
 X65962_s_at X65962 3769 cytochrome P450, subfamily IIC (mephenytoin 4- 5.47 down 0.00014 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 X67235_s_at X67235 3773 hematopoietically expressed homeobox 3.17 down 0.0045
 X67491_f_at X67491 3776 glutamate dehydrogenase 1 7.45 down 0.00019
 X68277_at X68277 3777 dual specificity phosphatase 1 6.68 down 0.0036
 X68679_s_at X68679 3779 complement factor H related 3, complement factor 38.22 down 0.00036
 X68733_ma1_at X68733 3781 alpha-1-antichymotrypsin 7.87 down 0.03266
 X72012_at X72012 3789 endoglin (Osler-Rendu-Weber syndrome 1) 4.2 down 0.005
 X72177_ma1_at X72177 3790 complement component 6 12.94 down 0.00011
 X75252_at X75252 3793 prostatic binding protein 3.78 down 0.00231
 X76105_at X76105 3794 death-associated protein 3.02 down 0.00944
 X76648_at X76648 3796 glutaredoxin (thioltransferase) 4 down 0.00211
 X76717_at X76717 3797 metallothionein 1L 8.09 down 0.00025
 X77548_at X77548 3798 nuclear receptor coactivator 4 3.76 down 0.00758
 X78706_at X78706 3801 carnitine acetyltransferase 4.65 down 0.00442
 X78992_at X78992 3802 butyrate response factor 2 (EGF-response factor 4.69 down 0.01995
 prion protein (p27-30) (Creutzfeldt-Jakob disease,
 X83416_s_at X83416 3811 Gerstmann-Strausler-Scheinker syndrome, fatal 3.28 down 0.00221
 3-hydroxy-3-methylglutaryl-Coenzyme A synthase
 X83618_at X83618 3813 2 (mitochondrial) 6.27 down 0.02099
 X85116_ma1_s_at X85116 3814 erythrocyte membrane protein band 7.2 6.37 down 0.00356
 X86401_s_at X86401 3815 glycine amidinotransferase (L-arginine:glycine 22.7 down 0
 X87344_cds10_r_at X87344 3817 EST 3.04 down 0.02779
 X95079_s_at X95079 3819 EST 29.82 down 0.00273
 X90999_at X90999 3820 hydroxyacyl glutathione hydrolase; glyoxalase 2 5.27 down 0.00047
 X91148_at X91148 3821 microsomal triglyceride transfer protein (large 5.91 down 0.00045
 X92720_at X92720 3826 phosphoenolpyruvate carboxykinase 2 7.6 down 0.00001
 X92744_at X92744 3827 defensin, beta 1 4.96 down 0.01804
 X94563_xpt2_r_at X94563 3831 EST 3.52 down 0.00928
 X95190_at X95190 3832 acyl-Coenzyme A oxidase 2, branched chain 12.81 down 0
 X95384_at X95384 3833 translational inhibitor protein p14.5 17.69 down 0.00048
 X95715_at X95715 3835 ATP-binding cassette, sub-family C (CFTR_atMRP), 6.78 down 0.00045
 X95876_at X95876 3836 G protein-coupled receptor 9 3.12 down 0.001 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 X96752_at X96752 3837 L-3-hydroxyacyl-Coenzyme A dehydrogenase, 4.94 down 0.00359
 X97324_at X97324 3839 adipose differentiation-related protein; adipophilin 5.97 down 0.04638
 X98337_s_at X98337 3840 complement factor H related 3, complement factor 13.5 down 0.00001
 Y00097_s_at Y00097 3844 annexin A6 3.4 down 0.00233
 Y00317_at Y00317 3845 UDP glycosyltransferase 2 family, polypeptide B4 18.34 down 0.00001
 Y00317_at Y00317 3845 UDP glycosyltransferase 2 family, polypeptide B4 8.97 down 0.00025
 Y00318_at Y00318 3846 I factor (complement) 10 down 0.00019
 Y00339_s_at Y00339 3847 carbonic anhydrase II 6.89 down 0
 Y00451_s_at Y00451 3848 aminolevulinate, delta-, synthase 1 10.52 down 0.00107
 Y08374_ma1_at Y08374 3853 chitinase 3-like 1 (cartilage glycoprotein-39) 3.5 down 0.04208
 Y08409_at Y08409 3854 thyroid hormone responsive SPOT14 (rat) 5.84 down 0.00455

Y09616_at Y09616 3857 carboxylesterase 2 (intestine, liver) 18.78 down 0.00026
 Y10032_at
 Y10032 3858 serum_atglucocorticoid regulated kinase 4.24 down 0.00148
 Y10659_at Y10659
 3859 interleukin 13 receptor, alpha 1 4.22 down 0.00061
 Y01659_at Y10659 3859 interleukin 13
 receptor, alpha 1 3.17 down 0.00095
 Y12711_at Y12711 3861 progesterone binding protein 14.83
 down 0.00285
 Z11559_at Z11559 3862 iron-responsive element binding protein 1 4.3 down
 0.00066
 Z11737_at Z11737 3863 flavin containing monooxygenase 4 3.84 down 0.00043

 Z11737_at Z11737 3863 flavin containing monooxygenase 4 3.67 down 0.00632
 Z11793_at
 Z11793 3864 selenoprotein P, plasma, 1 9.94 down 0.00021
 branched chain keto acid
 dehydrogenase E1,
 Z14093_at Z14093 3865 alpha polypeptide (maple syrup urine disease) 3.24
 down 0.00301
 Z20777_at Z20777 3866 EST 29.59 down 0.00044
 Z24459_ma1_at Z24459
 3869 mature T-cell proliferation 1 5.29 down 0.00001
 Z24725_at Z24725 3870 mitogen inducible
 2 7.9 down 0
 Z26491_s_at Z26491 3873 catechol-O-methyltransferase 3.08 down 0.00877

 aldo-keto reductase family 1, member D1 (delta 4-
 Z28339_at Z28339 3875 3-ketosteroid-5-beta-
 reductase) 24.66 down 0
 Z29481_at Z29481 3877 3-hydroxyanthranilate 3,4-dioxygenase 6.39
 down 0.00029
 Z29481_at Z29481 3877 3-hydroxyanthranilate 3,4-dioxygenase 3.64 down
 0.00096
 Z30425_at Z30425 3878 nuclear receptor subfamily 1, group I, member 3 26.64 down 0
 Table 6B. Down regulated in metastatic cancers versus normal sample set 2.
 <P>Affy ID Genbank
 Seq ID Known Gene Name Fold Change Direction Pvalue
 Z30425_at Z30425 3878 nuclear
 receptor subfamily 1, group I, member 3 7.88 down 0.000066
 Z31357_at Z31357 3880 cystein
 dioxygenase, type I 11.2 down 0.0001
 Z31690_s_at Z31690 3881 lipase A, lysosomal acid,
 cholesterol esterase 3.83 down 0.00103
 rc_Z38161_at Z38161 3884 EST 4.38 down 0.0011

 rc_Z38192_s_at Z38192 3885 EST 3.35 down 0.00184
 rc_Z38435_at Z38435 3890 ribosomal
 protein L21 3.12 down 0.03617
 rc_Z38777_f_at Z38777 3895 nuclear receptor binding factor-2
 3.28 down 0.022
 rc_Z39059_at Z39059 3899 EST 5.19 down 0.0014
 rc_Z39406_at Z39406
 3905 nuclear receptor co-repressor 1 4.18 down 0.00439
 rc_Z39431_at Z39431 3907 KIAA1086
 protein 3.68 down 0.0013
 rc_Z39476_at Z39476 3908 EST 5.9 down 0.00687

 rc_z39622_s_at Z39622 3910 EST 4.4 down 0.00001
 rc_Z39818_at Z39818 3912 EST 3.26 down
 0.00089
 rc_Z39833_at Z39833 3913 GTP-binding protein 16.89 down 0.00034

 rc_Z39976_at Z39976 3915 EST 5.76 down 0.00012
 rc_Z39978_at Z39978 3916 EST 3.56 down
 0.04051
 rc_Z40192_at Z40192 3918 EST 3.89 down 0.00223
 rc_Z40259_s_at Z40259
 3919 EST 8.18 down 0.00002
 rc_Z40305_at Z40305 3920 EST 6.45 down 0.00001

 rc_Z40715_at Z40715 3923 delta-6 fatty acid desaturase 18.68 down 0.0007
 rc_Z40902_at
 Z40902 3926 SEC14 (S. cerevisiae)-like 2 12.87 down 0.00001
 rc_Z41042_at Z41042 3928 EST
 3.63 down 0.00943
 Z47553_at Z47553 3939 flavin containing monooxygenase 5 6.17 down
 0.00011
 Z48199_at Z48199 3942 syndecan 1 4.43 down 0.00408
 Z48475_at Z48475 3943
 glucokinase (hexokinase 4) regulatory protein 13.84 down 0
 Z49269_at Z46269 3945 small
 inducible cytokine subfamily A (Cys-Cys), 18.46 down 0.00001
 Z49878_at Z49878 3946
 guanidinoacetate N-methyltransferase 13.96 down 0.00021
 Z69923_at Z69923 3948 HGF
 activator 11.37 down 0.00053
 Z80345_ma1_s_at Z80345 3951 acyl-Coenzyme A dehydrogenase,
 C-2 to C-3 5.93 down 0.0024
 Z84718_cds1_at Z84718 3952 EST 3.26 down 0.02252

 Z84721_cds2_at Z84721 3953 hemoglobin, zeta 8.77 down 0.01446 Table 7A. Up regulated in
 hepatocellular carcinoma versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene
 Name Fold Change Direction Pvalue
 rc_AA005358_at AA005358 14 EST 5.51 down
 0.00059
 rc_AA007395_s_at AA007395 17 alcohol dehydrogenase 4 (class II), pi polypeptide
 37.78 down 0.00939
 rc_AA07629_at AA07629 19 EST 5.56 down 0.0005

 rc_AA010205_at AA010205 23 EST 5.71 down 0.00014
 rc_AA010605_s_at AA010605 26 4-
 hydroxyphenylpyruvate dioxygenase 25.52 down 0.00855
 rc_AA010619_at AA010619 27 EST
 5.28 down 0.002
 rc_AA018922_s_at AA018922 40 core promoter element binding protein 3.39
 down 0.01801
 rc_AA035245_s_at AA035245 79 aldehyde oxidase 1 7.97 down 0.02387

 rc_AA035457_at AA035457 80 EST 3.41 down 0.00968
 rc_AA039335_s_at AA039335 89
 coagulation factor XII (Hageman factor) 5.33 down 0.03807
 rc_AA039616_at AA039616 90 EST

3.84 down 0.00997
 rc_AA046457_at AA046457 111 EST 3.05 down 0.02078

rc_AA046747_at AA046747 114 EST 4.77 down 0.00023
 rc_AA056482_at AA056482 141 EST
3.06 down 0.01313
 rc_AA057678_at AA057678 143 EST 6.63 down 0.00089

rc_AA069696_at AA069696 150 EST 3.07 down 0.01569
 rc_AA070191_at AA070191 154 EST
3.24 down 0.00216
 rc_AA074885_at AA074885 161 macrophage receptor with collagenous
structure 10.88 down 0.00087
 rc_AA076326_at AA076326 170 SEC14 (S. cerevisiae)-like 2 3.85
down 0.0349
 rc_AA076383_at AA076383 171 EST 4.65 down 0.00593
 rc_aa084668_at
AA084668 180 ubiquitin-like 3 3.31 down 0.02055
 rc_AA085987_s_at AA085987 183 UDP
glycosyltransferase 1 4.74 down 0.03035
 AA090257_at AA090257 190 superoxide dismutase 2,
mitochondrial 3.03 down 0.02774
 AA090439_at AA090439 192 ribosomal protein S6 5.11 down
0.01108
 rc_AA099225_at AA099225 206 EST 6.59 down 0.00064
 rc_AA100026μ
AA10026 211 EST 4.18 down 0.00567
 rc_AA112101_f_at AA112101 222 EST 4.36 down
0.03175
 rc_AA122345_f_at AA122345 238 glutamate dehydrogenase 1 3.75 down 0.01058

rc_AA129390_at AA129390 262 EST 4.03 down 0.00128
 rc_AA142849_at AA142849 306 EST
3.45 down 0.03495
 rc_aa147646_s_at AA147646 317 DKFZP586A0522 protein 3.19 down
0.00508 Table 7A.Up reglated in hepatocellular carcinoma versus normal sample set 2.
 <P>Affy
ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_AA150776_at
AA150776 330 EST 6.17 down 0.0004
 rc_AA151676_at AA151676 337 peptidyl arginine
deminase, type II 3.85 down 0.00875
 aldo-keto reductase famil6 7, member A2 (aflatoxin

rc_AA157799_at AA157799 348 aldehyde reductase) 3.8 down 0.00207
 rc_AA164586_s_at
AA164586 359 estrogen receptor 1 3.56 down 0.01231
 rc_AA167565_at AA167565 362 EST
3.81 down 0.04057
 rc_AA172372_at AA172372 370 EST 5.12 down 0.00032

rc_AA182030_at AA182030 387 EST 3.51 down 0.0403
 AA188921_at AA188921 393 similar to
Caenorhabidits elegans protein C42C1.9 3.38 down 0.00862
 rc_AA194997_s_at AA194997 412
EST 4.8 down 0.00153
 rc_AA196287_at AA196287 420 EST 4.86 down 0.01656

rc_AA210850_at A210850 431 EST 3.12 down 0.00288
 rc_AA223902_at AA223902 450 EST
4.22 down 0.01315
 rc_AA232114_s_at AA232114 463 epoxide hydrolase 2, cytoplasmic 6.18
down 0.00231
 rc_AA233152_at AA233152 467 EST 5.8 down 0.00272
 rc_AA233837_at
AA233837 474 EST 3.46 down 0.01365
 rc_AA235310_at AA235310 496 EST 7.08 down
0.04056
 rc_AA236401_at AA236401 510 EST 5.31 down 0.01787
 rc_AA236455_r_at
AA236455 52 EST 6.73 down 0.02418
 rc_AA236455_s_at AA236455 512 EST 5.1 down
0.00307
 rc_AA253216_at AA253216 561 EST 4.14 down 0.0014
 rc_AA253369_s_at
AA253369 563 EST 5.64 down 0.00478
 rc_AA256367_s_at AA256367 579 paraoxonase 3 8.37
down 0.902326
 rc_AA258350_at AA258350 592 EST 4.1 down 0.02962

rc_AA279676_s_at AA27O676 630 deoxyribonuclease I-like 3 10.52 down 0.00181

rc_AA282061_at AA282061 652 KIAA0962 protein 3.46 down 0.00025
 rc_AA282886_at
AA282886 663 EST 3.29 down 0.00025
 rc_AA284795_at AA284795 678
phosphatidylethanolamine N-methyltransferase 5.7 down 0.0004
 rc_AA285053_at AA285053
681 EST 5 down 0.00718
 rc_AA287122_at AA287122 686 EST 5.21 down 0.00523

rc_AA287566_at AA287566 690 K8IAA0187 gene product 6.99 down 0.00023 Table 7A.Up reglated
in hepatocellular carcinoma versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known
Gene Name Fold Change Direction Pvalue
 rc_AA291749_s_at AA291749 703 estrogen receptor
1 5.06 down 0.00044
 rc_AA297532_f_at AA297532 725 down 5.01 down 0.00745

rc_AA343142_at AA343142 751 EST 5.79 down 0.02747
 fatty-acid-Coenzyme A ligase, long-
chain 1, fatty-acid-
 rc_AA348922_s_at AA348922 758 Coenzyme A ligase, long0-chain 2 11.4
down 0.00848
 AA376875_at AA376875 770 monoamine oxidase A 3.45 down 0.00105

rc_AA377087_at AA377087 771 3EST 4.61 down 0.01616
 AA397841_at AA397841 780 EST
3.29 down 0.00825
 rc_AA398892_at AA398892 800 similar to yeast BET3 (S. cerevisiae) 4.33
down 0.01326
 AA400177_at AA400177 808 EST 3.21 down 0.03901
 rc_AA401376_at
AA401376 829 EST 3.39 down 0.01403
 rc_AA401562_s_at AA401562 830 EST 7.97 down
0.00527
 rc_AA402224_at AA402224 836 growth arrest and DNA-damage-inducible, gamma 3.66

down 0.0033
 rc_AA404487_at AA404487 851 EST 3.01 down 0.0059
 rc_AA417046_at AA417046 915 fatty-acid-Coenzyme A ligase, very long-chain 1 8.49 down 0.02476
 small inducible cytokine subfamily B (Cyx-X-Cys),
 rc_AA426640_at AA426640 969 member 14 (BRAK) 4.8 down 0.00539
 rc_AA428325_at AA428325 988 EST 4.09 down 0.02486
 rc_AA433946_at AA433946 1033 EST 10.24 down 0.00663
 rc_AA435746_f_at AA435746 1043 GTPase activating protein-like 4.21 down 0.03192
 rc_AA435985_at AA435985 1049 EST 3.86 down 0.01713
 AA442334_at AA442334 1069 EST 3.02 down 0.01936
 rc_AA446864_at AA446864 1095 EST 11.57 down 0.0001
 rc_AA448002_at AA448002 1113 putative type II membrane protein 14.14 down 0
 FXD domain-containing ion transport regulator 1
 rc_AA448300_at AA448300 1116 (phospholemman) 9.27 down 0.00108
 rc_AA450114_at AA450114 1131 EST 3.29 down 0.01171
 rc_AA450127_at AA450127 1132 growth arrest and DNA-damage-inducible, beta 3.37 down 0.00647
 rc_AA453988_at AA453988 1160 methionine adenosyltransferase I, alpha 7.78 down 0.02695
 rc_AA454733_s_at AA454733 1169 EST 5.73 down 0.00748
 rc_AA455367_at AA455367 1176 DKFZP586F1018 protein 3.47 down 0.00138 Table 7A.Up regulated in hepatocellular carcinoma versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 butyrobetaine (gamma), 2-oxoglutarate dioxygenase
 rc_AA455988_at AA455988 1184 (gamma-butyrobetaine hydroxylase) 12.51 down 0
 rc_AA458652_at AA458652 1202 EST 5.03 down 0.00065
 solute carrier family 22 (extraneuronal monoamine)
 rc_AA460012_at AA460012 1224 transporter, member 3 3.73 down 0.0313
 rc_AA460449_at AA460449 1228 EST 3.53 down 0.01247
 rc_AA460661_at AA460661 1229 EST 5.46 down 0.00151
 rc_AA461444_at AA461444 1239 EST 3.19 down 0.02844
 rc_AA465233_s_at AA465233 1269 succinate-CoA ligase, GDP-forming, beta subunit 3.19 down 0.00036
 rc_AA477119_at AA477119 1289 EST 4.62 down 0.00072
 AA477919_at AA477919 1293 EST 3.9 down 0.00265
 rc_AA478298_s_at AA478298 1297 adipose specific 2 5.29 down 0.00943
 rc_AA480991_s_at AA480991 1323 EST 4.83 down 0.03498
 AA486511_at AA486511 1349 EST 3.9 down 0.0149
 rc_AA490620_at AA490620 1378 EST 6.25 down 0.03613
 rc_AA599472_at AA599472 1451 succinate-CoA ligase, GDP-forming, beta subunit 3.31 down 0.02619
 rc_AA599814_at AA599814 1456 EST 4.09 down 0.00235
 rc_AA599937_s_at AA599937 1458 insulin-like growth factor-binding protein 4 6.31 down 0.0477
 rc_AA608802_at AA608802 1470 EST 3.44 down 0.01709
 rc_AA608837_at AA608837 1472 EST 5.15 down 0.00005
 rc_AA609519_at AA609519 482 EST 5.23 down 0.00068
 rc_AA609537_s_at AA609537 1483 hepatic leukemia factor 4.88 down 0.00118
 rc_AA621131_at AA621131 1513 EST 4.57 down 0.03867
 rc_AA621209_at AA621209 1516 similar to Caenorhabditis elegans proteinC42C1.9 4.01 down 0.00563
 C02386_s_at c02386 1561 hypothetical protein 3.66 down 0.0673
 C02460_at C02460 1562 EST 3.92 down 0.03073
 rc_C20653_at C20653 1578 EST 4.32 down 0.00718
 rc_C20810_at C20810 1579 EST 3.57 down 0.02116
 rc_C21130_at C21130 1583 EST 3.24 down 0.03355
 cytochrome p450, subfamily IIA (naphthodiol oxidase),
 D00003_at D00003 1586 polypeptide 3 9.46 down 0.00001 Table 7A.Up regulated in hepatocellular carcinoma versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 cytochrome P450, subfamily IIA (naphthodiol oxidase),
 D00003_s_at D00003 1586 polypeptide 3 6.8 down 0.01328
 cytochrome P450, subfamily IIA (naphthodiol oxidase),
 polypeptide 3, cytochrome P450, subfamily IIA
 (naphthodiol oxidase), polypeptide 5, cytochrome P450,
 D00408_s_at D00408 1589 subfamily IIA, polypeptide 7 3.58 down 0.02048
 D10040_at D10040 1593 fatty-acid-Coenzyme A ligase, longchain 2 4.15 down 0.02947
 rc_D11756_f_at D11756 1596 EST 4.08 down 0.02972
 cytochrome P450, subfamily IVF, polypeptide
 2, cytochrome P450, subfamily IVF, polypeptide 3
 D12620_s_at D12620 1601 (leukotriene B4 omega hydroxylase) 6.03 down 0.03947
 cytochrome p450, subfamily IVF, polypeptide
 2, cytochrome p450, subfamily IVF, polypeptide 3
 D12620_s_at D12620 1601 (leukotriene B4 omega hydroxylase) 4.7 down 0.04091
 D13243_s_at D13243 1602 pyruvate kinase, liver and RBC 5.58 down 0.04029
 D13705_s_at D13705 1610 cytochrome P450, subfamily IVA, polypeptide 11 3.3 down

0.0051
 D14012_s_at D14012 1612 HGF activator 7.27 down 0.00145
 D1628_s_at D31628 1646 4hydroxyphenylpyruvate dioxygenase 13.18 down 0.02064
 rc_D45529_at D45529 1662 EST 3.01 down 0.03105
 D49357_at D49357 1665 methionine adenosyltransferase I, alpha 4.85 down 0.04435
 rc_D62518_at D62518 1708 EST 5.96 down 0.00027
 ficolin (collagen/fibrinogen domain-containing lectin) 2
 D63160_at D63160 1709 (hucolin) 3.72 down 0.00312
 D78011_at D78011 1717 dihydropyrimidinase 5.54 down 0.0312
 D78725_at D78725 1720 KIAA0914 gene product 3.19 down 0.01083
 D79276_at D79276 1722 succinate-CoA ligase, GDP-forming, beta subunit 4.34 down 0.00836
 D90042_at D90042 1767 N-acetyltransferase 2 (arylamine N-acetyltransferase) 3.79 down 0.00697
 rc_F02028_at F02028 1774 EST 3.15 down 0.00902
 rc_F00245_at F02245 1776 monomamine oxidase A 3.51 down 0.01692
 matrix metalloproteinase 2 (gelatinase A, 72kD
 rc_F03969_at F03969 1785 gelatinase, 72kD type IV collagenase) 3.36 down 0.01685 Table 7A. Up regulated in hepatocellular carcinoma versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_Ho2855_at H02855 1832 EST 4.29 down 0.0138
 rc_H05704_s_at H05704 1848 EST 3.07 down 0.00363
 rc_H06935_s_at H06935 1855 electron-transferring-flavoprotein dehydrogenase 4.04 down 0.01498
 rc_H08102_at H08102 1858 breast cell glutaminase 12.85 down 0.0424
 rc_H09317_at H09317 1864 EST 3.2 down 0.00914
 methylenetetrahydrofolate dehydrogenase (NADP+
 dependent), methenyltetrahydrofolate cyclohydrolase,
 rc_H10779_s_at H10779 1872 formyltetrahydrofolate synthetase 3.09 down 0.0496
 rc_H20543_at H20543 1897 DKFZP586B1621 protein 13.06 down 0.00218
 rc_h27330_at H27330 1909 EST 3.37 down 0.01318
 rc_H29568_at H29568 1914 EST 5 down 0.00426
 rc_H55759_at H55759 1949 EST 4.36 down 0.0398
 rc_H57060_s_at H57060 1954 EST 7.57 down 0.0875
 rc_H57816_at H57816 1957 EST 3.09 down 0.01327
 rc_H58673_at H58673 1959 EST 15.49 down 0.00002
 rc_h58692_s_at H58692 1960 formyltetrahydrofolate dehydrogenase 20.18 down 0.00485
 rc_H59136_at H59136 1962 EST 6.63 down 0.00033
 rc_H62212_at H62212 1969 telomeric repeat binding factor 2 3.23 down 0.00513
 H66367_at H66367 1977 EST 3.84 down 0.00133
 rc_H66840_at H66840 1978 EST 3.34 down 0.01884
 rc_H77597_f_at H77597 2000 metallothionein 1H 9.01 down 0.00022
 ficolin (collagen/fibrinogen domain-containing) 3 (H akata
 rc_H80901_s_at H80901 2005 antigen) 18.59 down 0
 rc_H81070_f_at H81070 2006 RNA helicase-related protein 39.64 down 0.00002
 rc_H87765_at H87765 2017 KIAA0626 gene product 3.94 down 0.00123
 H93246_s_at H93246 203 EST 4.14 down 0.00058
 rc_H93381_at H93381 2036 EST 8.62 down 0.01271
 rc_H99727_at H99727 2080 adipose differentiation-related protein; adipophilin 3.91 down 0.00325
 HG1428-HT1428_s_at HG1428-HT1428 hemoglobin, beta 8.98 down 0.02071
 HG2379-HT3996_s_at HG2379-HT3996 serine hydroxymethyltransferase 1 (soluble) 3.81 down 0.01837
 HG2730-HT2827_s_at HG2730-HT2827 fibrinogen, A alpha polypeptide 3.84 down 0.00795 Table 7A. Up regulated in hepatocellular carcinoma versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 HG2730-HT2828_s_at HG2730-HT2828 fibrinogen, A alpha polypeptide 3.62 down 0.01013
 HG2841-HT2968_s_at HG2841-HT2968 albumin 4.62 down 0.00552
 HG4533-HT4938_at HG4533-HT4938 protease inhibitor 4 (kallistatin) 3.35 down 0.01605
 J02843_at J02843 2088 cytochrome P450, subfamily IIE (ethanol-inducible) 6.18 down 0.01308
 solute carrier family 2 (facilitated glucose transporter),
 J03810_at J03810 2099 member 2 3.6 down 0.02376
 J03910_rna1_at J03910 2101 EST 18.13 down 0.00119
 J04093_s_at J04093 2106 UDP glycosyltransferase 1 3.28 down 0.02286
 cytochrome P450, subfamily IIIA (naphthalene oxidase),
 J0449_at J0449 2110 polypeptide 3 5.07 down 0.01733
 J05158_at J05158 2117 carboxypeptidase N, polypeptide 2, 83kD 3.37 down 0.01156
 J05428_at J05428 2120 UDPglycosyltransferase 2 family, polypeptide B7 4.86 down 0.03414
 coagulation factor IX (plasma thromboplastin component,
 K02402_at K02402 2125 Christmas disease, hemophilia B) 6.64 down 0.04082
 K02766_at K02766 2126 complement component 9 5.03 down 0.0433
 cytochrome P450, subfamily IIA (phenobarbital-inducible),
 K03192_f_at K03192 2127 polypeptide 6 14.19 down 0.0307

cytochrome P450, subfamily IIA (phenobarbital-inducible),
 K03192_f_at K03192 2127 polypeptide 6 8.02 down 0.03483
 low density lipoprotein receptor (familial
 L00352_at L00352 2131 hypercholesterolemia) 3.3 down 0.03487
 cytochrome P450, subfamily I (aromatic compound-
 L00389_f_at L00389 2132 inducible), polypeptide 2 3.87 down 0.00844
 L04751_at L04751 2138 cytochrome P450, subfamily IVA, polypeptide 11 8.13 down 0.02065
 L05144_at L05144 2139 phosphoenolpyruvate carboxykinase 1 (soluble) 4 down 0.021
 fatty-acid-Coenzyme A ligase, long-chain 1,fatty-acid-
 L09229_s_at L09229 2150 Coenzyme A ligase, long-chain 2 4.5 down 0.01347
 L11931_at L11931 2159 serine hydroxymethyltransferase 1 (soluble) 3.74 down 0.0056
 L12760_s_at L12760 2162 phosphoenolpyruvate carboxykinase 1 (soluble) 6.06 down 0.01005
 cytochrome P450, subfamily IIC (mephenytoin 4-
 L16883_s_at L16883 2166 hydroxylase), polypeptide 9 5.85 down 0.04368 Table 7A. Up regulated in hepatocellular carcinoma versus normal sample set 2.
 <P>Affy ID Genbank SeqID Known Gene Name Fold Change Direction Pvalue
 solute carrier family 10 (sodium/bile acid cotransporter
 L21893_at L21893 2176 family), member 1 5.23 down 0.03367
 L27050_at L27050 2186 apolipoprotein F 4.18 down 0.04901
 L32140_at L32140 2192 afamin 5.39 down 0.02767
 M10942_at M10942 2233 mealllothionein 1E (functional) 4.05 down 0.01412
 M10943_at M10943 2234 metallothionein 1F (functional) 6.23 down 0.00007
 M13143_at M13143 2249 kallikrein B plasma, (Fletcher factor) 1 3.04 down 0.008
 M14777-s_at M14777 2263 glutathione S-transferase A2,glutathione S-transferase A3 13.23 down 0.03224
 M16594_at M16594 2272 glutathione S-transferase A2 5.42 down 0.03813
 M16750_s_at M16750 2273 pim-1 oncogene 3.07 down 0.02391
 M16974-s_at M16974 2277 complemen component 8, alpha polypeptide 10.85 down 0.02313
 m25079_s_at M25079 2305 hemoglobin, beta 4.31 down 0.01567
 M26393_s_at M26393 2309acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain 4.3 down 0.02294
 M29873_s_at M29873 2318 cytochrome P450, subfamily IIB (phenobarbital-inducible) 17.92 down 0.01469
 M29874_s_at M29874 2319 cytochrome P450, subfamily IIB (phenobarbital-inducible) 8.13 down 0.01604
 M30185_at M30185 2321 cholesteryl ester transfer protein, plasma 3.82 down 0.00131
 M30185_at M30185 2321 cholesteryl ester transfer protein, plasma 3.31 down 0.00109
 cytochrome P450, subfamily I (aromatic compound-
 M31667_f_at M31667 2331 inducible), polypeptide 2 4.47 down 0.01116
 cytochrome P450, subfamily IIA (phenobarbital-inducible),
 M33317_f_at M33317 2338 polypeptide 7 11.47 down 0.02611
 M34276_at M34276 2341 plaswminogen 3.08 down 0.02754
 M57731_s_at M57731 2359 GRO2 oncogene 3.16 down 0.02204
 cytochrome P450, subfamily IIC (mephenytoin -4
 M61854-s_at M61854 2370 hydroxylase) 3.45 down 0.02949
 M63967_at M63967 2378 aldehydr dehydrogenase 5 3.88 down 0.00274
 M68840_at M68840 2388 monoamine oxidase A 3.1 down 0.01953 Table 7A. Up regulated in hepatocellular carcinoma versus normal sample set 2.
 <P>Affy ID Genbank Seq I Known Gene Name Fold Change Direction Pvalue
 M68895_rna1_at M68895 2390 alcohol dehydrogenase 6 (class V) 3.21 down 0.02095
 M72885_rna1-s_at M72885 2393 putative lymphocyte G0/G1 switch gene 3.34 down 0.02943
 M76665_at M76665 2398 hydroxysteroid (11-beta) dehydrogenase 1 6.06 down 0.01317
 M81349_at M81349 2405 serum amyloid A4, constitutive 10.97 down 0.01946
 M83652_s_at M83652 2408 properidin P factor, complement 6 down 0.00002
 M83772_at M83772 2409 flavin containing monooxygenase 3 5.14 down 0.02023
 insulin-like growth factor binding protein, acid labile
 M86826_at M86826 2413 subunit 3.75 down 0.01157
 M93405_at M93405 2424 methylmalonate-semialdehyde dehydrogenase 3.09 down 0.03285
 M94065-s_at M94065 2425 dihydroorotate dehydrogenase 7.87 down 0.0011
 M94065_at M94065 2425 dihydroorotate dehydrogenase 3.61 down 0.00229
 M95585_s_at M95585 2430 hepatic leukemia factor 3.36 down 0.00492
 transducin-like enhancer of split 4, homlg of Drosophila
 M99439_at M99439 2438 E(sp1) 4.82 down 0.00121
 rc_N22404_at N22404 2450 EST 3.44 down 0.02267
 rc_N22938_s_at N22938 2453 serum amyloid A4, constitive 4.91 down 0.01918
 rc_N29353_at N29353 2477 kynurenine 3-monooxygenase (kynurenine 3-hydroxylase) 3.44 down 0.01212
 rc_N29764_at N29764 2482 EST 4.48 down 0.013

rc_N31741_at N31741 2489 serine hydroxymethyltransferase 1 (soluble) 5.66 down 0.00212

rc_N34804_at N34804 2497 DKFZP434J214 protein 3.97 down 0.0175
 rc_N39163_at N39163
2509 metallothionein 1L 4.3 down 0.03917
 rc_N39201_at N39201 2510 protease inhibitor 4
(kallistatin) 4.79 down 0.02015
 rc_N49902_at N49902 2540 EST 3.02 down 0.00951

rc_N51117_at N51117 2544 EST 8.17 down 0.00105
 rc_N51773_at N51773 2549 EST 6.92
down 0.01839
 LIM protein (similar to rat protein kinase C-binding
 rc_N52771_at N52771
2552 enigma) 3.670 down 0.01102
 rc_N52322_at N52322 2553 EST 4.58 down 0.02077

rc_N54053_at N54053 2561 secreted phosphoprotein 2, 24kD 12.87 down 0.01821

rc_N54417_s_at N54417 2567 fibrinogen, A alpha polypeptide 6.47 down 0.00733 Table 7A. Up
regulated in hepatocellular carcinoma versus normal sample set 2
 Affy ID Genbank Seq ID Known
Gene Name Fold Change Direction Pvalue
 rc_N54429_at N54429 2568 EST 6.85 down
0.03334
 rc_N54950_s_at N54950 2573 ketohexokinase (fructokinase) 6.47 down 0.0223

N57464_at N57464 2576 CCAAT/enhancer binding protein (C/EBP), delta 4.87 down 0.00111

rc_N57934_s_at N57934 2577 formiminotransferase cyclodeaminase 3.28 down 0.01555

rc_N58009_at N58009 2578 formiminotransferase cyclodeaminase 8.52 down 0.01808

rc_N59550_at N59550 2588 EST 4.78 down 0.02924
 rc_N63391_at N63391 2600 EST 3.87
down 0.02935
 rc_N63845_at N63845 2605 phytanoyl-CoA hydroxylase (Refsum disease) 6.82
down 0.00369
 enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A
 rc_N64036_s_at
N64036 2607 dehydrogenase 6.12 down 0.00476
 rc_N65959_at N65959 2612 EST 3.38 down
0.00785
 rc_N66066_at N66066 2613 EST 4.33 down 0.0184
 rc_N67105_at N67105 2624
EST 4.69 down 0.00194
 rc_N68596_s_at N68596 2636 betaine-homocysteine methyltransferase
10.46 down 0.01971
 rc_N70358_s_at N70358 2657 growth hormone receptor 8.47 down
0.00816
 slute carrier family 10 (sodium/bile acid cotransporter
 rc_N70966_s_at N70966
2663 family), member 1 10.8 down 0.02894
 rc_N73543_at N73543 2675 EST 4.64 down
0.03981
 rc_N74025_at N74025 2685 deiodinase, iodothyronine, type I 8.18 down 0.01363

N77326_at N77326 29696 EST 4.08 down 0.00768
 rc_N80129_i_at N80129 2703
metallothionein 1L 26.87 down 0.00999
 rc_N80129_f_at N80129 2703 metallothionein 1L 11.48
down 0.00167
 rc_N90584_at N90584 2714 EST 3.36 down 0.01561
 N91087_at N91087
2717 EST 3.66 down 0.00725
 N99542_at N99542 2747 orosomucoid 1 3.53 down 0.00607

rc_R01023_s_at R01023 2752 glucokinase (hexokinase 4) regulatory protein 4.56 down 0.04036

rc_R08564_at R08564 2780 plasminogen-like 8.77 down 0.01284
 rc_R09053_at R09053 2783
EST 3.45 down 0.03074
 rc_R12472_at R12472 2789 EST 12.09 down 0.02379

rc_R22905_at R22905 2801 EST 4.31 down 0.01744
 rc_R40395_s_at R40395 2841 lecithin-
cholesterol acyltransferase 12.85 down 0.01334 Table 7A. Up regulated in hepatocellular carcinoma
versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change
Direction Pvalue
 rc_R40492_at R40492 2842 EST 6.4 down 0.00527
 rc_R40899_f_at
R40899 2844 glycine receptor, beta 4.84 down 0.02369
 rc_R43799_at R43799 2851 EST 3.93
down 0.005
 rc_R49602_at R49602 2885 EST 16.17 down 0.00279
 rc_R59722_at R59722
2916 EST 6.24 down 0.02361
 rc_R65593_s_at R65593 2935 kynurenine 3-monooxygenase
(kynurenine 3-hydroxylase) 6.6 down 0.01982
 rc_R66002_at R66002 2936 EST 4.33 down
0.00789
 R69417_at R69417 2942 EST 6.43 down 0.00778
 rc_R73816_at R73816 2961
EST 7.05 down 0.01287
 R77628_at R77628 2966 insulin induced gene 1 5.51 down 0.0404

R79750_at R79750 2971 EST 4.89 down 0.00695
 R80048_at R80048 2972 EST 3.61 down
0.01209
 rc_R89811_s_at R89811 2980 HGF activator 13.29 down 0.00148
 rc_R92475_s_at
R92475 2987 flevin containing monooxygenase 3 6.46 down 0.02269
 rc_R93714_at R93714
2992 fetuin B 4.65 down 0.03704
 R93776_s_at R93776 2993 EST 5.55 down 0.00084

rc_R94674_s_at R94674 2996 EST 4.58 down 0.0047
 cytochrome P450, subfamily VIIIB (sterol
12-alpha-
 rc_R97419_at R97419 3004 hydroxylase), polypeptide 1 19.3 down 0.00807

R98073_at R98073 3009 EST 8.37 down 0.01436
 rc_R99591_at R99591 3016 CD5 antigen-like
(scavenger receptor cysteine rich family) 7.41 down 0.00043
 aldo-keto reductase family 1,
member C4 (chlordencome
 reduclase; 3-alpha hydroxysteroid dehydrogenase, type I;

S68287_at S68287 3025 dihydrodiol dehydrogenase 4) 5.04 down 0.02895
 S70004_at S70004
 3029 glycogen synthase 2 (liver) 5.13 down 0.00183
 S77356_at S77356 3034 EST 3.56 down
 0.03874
 rc_T10264_s_at T10264 3051 EST 3.26 down 0.01718
 rc_T16484_s_at T16484
 3071 EST 4.78 down 0.00009
 rc_T40936_at T40936 3118 EST 4.62 down 0.02844 Table 7A. Up
 regulated in hepatocellular carcinoma versus normal sample set 2.
 <P>Affy ID Genbank Seq ID
 Known Gene Name Fold Change Direction Pvalue
 rc_T40995_f_at T40995 3119 alcohol
 dehydrogenase 3 (class I), gamma polypeptide 3.42 down 0.00957
 rc_T41047_s_at T41047 3120
 EST 3.08 down 0.00553
 rc_T41232_at T41232 3122 EST 3.14 down 0.02012

 rc_T47778_s_at T47778 3127 fibrinogen, A alpha polypeptide 3.33 down 0.00637

 rc_T48075_f_at T48075 3130 hemoglobin, alpha 1 35.75 down 0.00471
 rc_T48278_at T48278
 3132 EST 24.1 down 0.00595
 rc_T51150_at T51150 3137 EST 8.65 down 0.00553
 solute
 carrier family 22 (extraneuronal monoamine
 rc_T51617_at T51617 3138 transporter), member 3
 6.16 down 0.04198
 rc_T52813_s_at T52813 3142 putative lymphocyte G0/G1 switch gene 5.4
 down 0.02021
 rc_T56281_f_at T56281 3151 RNA helicase-related protein 14.64 down
 0.00027
 T57140_s_at T57140 3152 paraoxonase 3 8.47 down 0.01048
 rc_T58756_at
 T58756 3156 EST 16.61 down 0
 rc_T61256_s_at T61256 3162 ketohexokinase (fructokinase)
 3.56 down 0.04957
 rc_T61649_f_at T61649 3165 superoxide dismutase 2, mitochondrial 4.08
 down 0.0389
 ficolin (collagen/fibrinogen domain-containing) 3 (Hakata
 rc_T63364_at
 T63364 3170 antigen) 6.27 down 0.00455
 rc_T64575_s_at T64575 3172 EST 3.16 down
 0.01855
 rc_T67931_at T67931 3184 fibrinogen, B beta polypeptide 17.25 down 0.00128

 T68510_at T68510 3187 EST 3.19 down 0.01504
 rc_T68711_at T68711 3188 EST 35.98 down
 0.0003
 rc_T68873_f_at T68873 3190 metallothionein 1L 13.68 down 0.00593

 carboxylesterase 1 (monocyte/macrophage serine
 rc_T68878_f_at T68878 3191 esterase 1) 4.18
 down 0.02474
 rc_T69305_at T69305 3197 EST 15.87 down 0.02258
 rc_T72502_at T72502
 3208 EST 4.74 down 0.00404
 rc_T72906_at T72906 3210 EST 4.91 down 0.00512

 rc_T74542_s_at T74542 3215 UDP glycosyltransferase 2 family, polypeptide B10 7.19 down
 0.011
 rc_T74608_at T74608 3216 hydroxyacid oxidase (glycolate oxidase) 1 6.1 down
 0.00249
 rc_T78433_s_at T78433 3220 glycogen synthase 2 (liver) 5.74 down 0.00949

 T83397_at T83397 3233 phytanoyl-CoA hydroxylase (Refsum disease) 8.03 down 0.02173 Table 7A.
 Up regulated in hepatocellular carcinoma versus normal sample set 2.
 <P>Affy ID Genbank Seq ID
 Known Gene Name Fold Change Direction Pvalue
 rc_T87174_at T87174 3240 EST 3.46 down
 0.00026
 T95813_f_at T95813 3262 KIAA1051 protein 20.36 down 0.01361

 rc_T98199_i_at T98199 3267 EST 4.05 down 0.00753
 rc_T98676_at T98676 3269 EST 11.15
 down 0.0323
 U02388_at U02388 3278 cytochrome P450, subfamily IVF, polypeptide 2 4.4 down
 0.00761
 U06641_s_at U06641 3287 UDP glycosyltransferase 2 family, polypeptide B15 6.37
 down 0.01594
 U08006_s_at U08006 3290 complement component 8, alpha polypeptide 3.96
 down 0.04272
 U08021_at U08021 3291 nicotinamide N-methyltransferase 3.63 down
 0.03726
 U20530_at U20530 3322 secreted phosphoprotein 2, 24kD 5.31 down 0.01119

 U21931_at U21931 3326 fructose-bisphosphatase 1 3.17 down 0.0143
 cytochrome P450,
 subfamily IIA (phenobarbital-inducible),
 U22029_f_at U22029 3327 polypeptide 7 11.85 down
 0.03538
 solute carrier family 6 (neurotransmitter transporter,
 U27699_at U27699 3340
 betaine/GABA), member 12 3.65 down 0.00381
 U50196_at U50196 3377 adenosine kinase 3.03
 down 0.00975
 U50929_at U50929 3380 betaine-homocysteine methyltransferase 8.04 down
 0.0188
 U51010_s_at U51010 3381 nicotinamide N-methyltransferase 4.69 down 0.03099

 U56814_at U56814 3393 deoxyribonuclease I-like 3 17.69 down 0.00007
 U56814_at U56814
 3393 deoxyribonuclease I-like 3 5.75 down 0.00152
 U65932_at U65932 3405 extracellular matrix
 protein 1 3.18 down 0.00575
 U95090_at U95090 3464 nephrosis 1, congenital, Finnish type
 (nephrin) 4.63 down 0.01595
 W07723_at W07723 3471 EST 3.51 down 0.00026

 W26996_at W26996 3484 EST 4.46 down 0.00734
 W28414_at W28414 3490 EST 4.06 down
 0.00083
 W28798_at W28798 3492 phosphodiesterase 6A, cGMP-specific, rod, alpha 3.33 down
 0.00222
 W28944_at W28944 3494 EST 6.9 down 0.01014
 rc_W44745_at W44745 3520

EST 3.87 down 0.01051
 rc_W45560_at W45560 3525 EST 3.48 down 0.0179
 W55903_at W55903 3546 adipose differentiation-related protein; adipophilin 5.64 down 0.00014
 rc_W63728_at W63728 3565 EST 3.86 down 0.00288
 rc_W67147_at W67147 3568 deleted in liver cancer 1 4.37 down 0.00069 Table 7A. Up regulated in hepatocellular carcinoma versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_W72044_at W72044 3580 insulin induced gene 1 3.1 down 0.03445
 oxidative 3 alpha hydroxysteroid dehydrogenase; retinol
 rc_W72382_at W72382 3584 dehydrogenase 9.89 down 0.03091
 rc_W73601_at W73601 3592 EST 3.45 down 0.01382
 rc_W73818_at W73818 3593 EST 3.47 down 0.00927
 rc_W81552_at W81552 3615 EST 12.97 down 0.00244
 rc_W86075_at W86075 3624 EST 6.04 down 0.01486
 rc_W86600_at W86600 3628 EST 3.67 down 0.04208
 rc_W87532_at W87532 3634 putative glycine-N-acyltransferase 5.5 down 0.00739
 rc_W87781_at W87781 3636 EST 4.02 down 0.00284
 rc_W88946_at W88946 3639 putative glycine-N-acyltransferase 25.28 down 0.00221
 rc_W95041_at W95041 3662 EST 4.22 down 0.01005
 X02176_s_at X02176 3672 complement component 9 3.84 down 0.01793
 X06562_at X06562 3686 growth hormone receptor 4.8 down 0.00507
 X06985_at X06985 3689 heme oxygenase (decycling) 1 3.34 down 0.00045
 X13277_at X13277 3698 D-amino-acid oxidase 3.22 down 0.01753
 cytochrome P450, subfamily IIA (phenobarbital-inducible),
 X13930_f_at X13930 3700 polypeptide 6 8.1 down 0.0219
 acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3-
 X14813_at X14813 3705 oxoacyl-Coenzyme A thiolase0 3.53 down 0.00059
 X16260_s_at X16260 3710 inter-alpha (globulin) inhibitor, H1 polypeptide 3.76 down 0.00291
 X16349_s_at X16349 3712 sex hormone-binding globulin 6.61 down 0.00008
 X54380_at X54380 3730 pregnancy-zone protein 7.71 down 0.00069
 X56411_ma1_at X56411 3737 alcohol dehydrogenase 4 (class II), pi polypeptide 9.87 down 0.01416
 X58022_at X58022 3747 corticotropin releasing hormone-binding protein 4.09 down 0.00076
 X63359_at X63359 3759 UDP glycosyltransferase 2 family, polypeptide B10 4.26 down 0.01725
 X64177_f_at X64177 3763 metallothionein 1H 3.26 down 0.03928
 X67491_f_at X67491 3776 glutamate dehydrogenase 1 4.06 down 0.00273
 X72177_ma1_at X72177 3790 complement component 6 4.25 down 0.01598
 X76717_at X76717 3797 metallothionein 1L 5.64 down 0.00215
 X90579_s_at X90579 3819 EST 4.26 down 0.04759 Table 7A. Up regulated in hepatocellular carcinoma versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 X95190_at X95190 3832 acyl-Coenzyme A oxidase 2, branched chain 6.22 down 0.00162
 X97324_at X97324 3839 adipose differentiation-related protein; adipophilin 3.72 down 0.00202
 Y00317_at Y00317 3845 UDP glycosyltransferase 2 family, polypeptide B4 4.63 down 0.02986
 Z20777_at Z20777 3866 EST 15.73 down 0.00147
 aldo-keto reductase family 1, member D1 (delta 4-3-
 Z28339_at Z28339 3875 ketosteroid-5-beta-reductase) 8.03 down 0.00853
 lipase A, lysosomal acid, cholesterol esterase (Wolman
 Z31690_s_at Z31690 3881 disease) 3.29 down 0.00161
 rc_Z40259_s_at Z40259 3919 EST 4.47 down 0.00093
 rc_Z40305_at Z40305 3920 EST 4.09 down 0.00096
 rc_Z40902_at Z40902 3926 SEC14 (S. cerevisiae)-like 2 4.97 down 0.04627
 rc_Z41042_at Z41042 3928 EST 3.37 down 0.00703
 Z48475_at Z48475 3943 glucokinase (hexokinase 4) regulatory protein 4.6 down 0.01693
 small inducible cytokine subfamily A (Cys-Cys), member
 Z49269_at Z49269 3945 14 7.24 down 0.01047
 Z69923_at Z69923 3948 HGF activator 3.95 down 0.00012
 Z80345_ma1_s_at Z80345 3951 acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain 3.21 down 0.04734
 Z84721_cds2_at Z84721 3953 hemoglobin, zeta 7.39 down 0.01921 Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_AA001504_f_at AA001504 2 EST 4.44 up 0.03077
 rc_AA005262_at AA005262 13 EST 3.09 up 0.0064
 KIAA1080 protein; Golgi-associated, gamma-adaptin ear
 rc_AA007507_at AA007507 18 containing, ARF-binding protein 2 5.23 up 0.00159
 rc_AA010065_s_at AA010065 22 CDC28 protein kinase 2 3.71 up 0.00432
 rc_AA011209_s_at AA011209 30 melanoma-associated antigen recognised by T 6.45 up 0.00088
 rc_AA011679_at AA011679 32 EST 3.08 up

0.03649
 rc_AA018346_at AA018346 38 EST 3.69 up 0.04582
 rc_AA021549_at AA021549 42 EST 3.17 up 0.00158
 rc_AA022623_at AA022623 44 EST 3.27 up 0.01556
 rc_AA024658_at AA024658 47 ribosomal protein S19 7.55 up 0.00592
 rc_AA024776_at AA024776 48 EST 3.44 up 0.00334
 rc_AA025166_s_at AA025166 50 fusion, derived from t (12;16) malignant liposarcoma 3.17 up 0.00009
 rc_AA026356_at AA026356 57 EST 5.04 up 0.02483
 rc_AA027833_i_at AA027833 59 EST 5.02 up 0.01123
 rc_AA029288_at AA029288 65 EST 3.36 up 0.04908
 rc_AA031814_at AA031814 70 KIAA0958 protein 3.07 up 0.00681
 rc_AA037058_s_at AA037058 84 laminin, gamma 1 (formerly LAMB2) 4.11 up 0.02264
 rc_AA037433_at AA037433 86 EST 4.9 up 0.0194
 rc_AA037766_at AA037766 87 EST 3.63 up 0.0328
 rc_AA040465_at AA040465 95 EST 3.63 up 0.01806
 AA043111_s_at AA043111 97 EST 6.36 up 0.0005
 rc_AA043959_at AA043959 101 tropomyosin 4 4.37 up 0.01641
 rc_AA045365_at AA045365 106 EST 3.17 up 0.0149
 rc_AA046103_at AA046103 109 EST 3.75 up 0.02893
 rc_AA046410_s_at AA046410 110 EST 3.18 up 0.00797
 rc_AA046745_at AA046745 113 Wolf-Hirschhorn syndrome candidate 1 3.33 up 0.00648
 rc_AA047379_s_at AA047379 119 karyopherin (importin) beta 1 3.15 up 0.01572
 rc_AA047704_at AA047704 120 EST 3.2 up 0.0029
 rc_AA052941_at AA052941 121 EST 3.36 up 0.00088
 rc_AA053662_f_at AA053662 129 EST 3.3 up 0.00558 Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_AA053680_at AA053680 130 high-mobility group protein 2-like 1 4.07 up 0.03144
 rc_AA055892_at AA055892 134 EST 3.02 up 0.04984
 rc_AA055896_at AA055896 135 collagen, type V, alpha 1 10.87 up 0.00907
 rc_AA070206_at AA070206 155 EST 3.15 up 0.03914
 rc_AA070485_at AA070485 156 interleukin 13 receptor, alpha 1 3.19 up 0.03465
 rc_AA070827_at AA070827 157 EST 4.37 up 0.02617
 AA071387_at AA071387 158 jumping translocation breakpoint 3.31 up 0.0001
 rc_AA074162_s_at AA074162 159 superkiller viralicidic activity 2 (S. cerevisiae homolog)- 3.23 up 0.00642
 rc_AA076138_at AA076138 167 H2A histone family, member Y 3.75 up 0.01442
 rc_AA086071_at AA086071 184 chromosome-associated polypeptide c 3.77 up 0.01993
 kangai 1 (suppression of tumorigenicity 6, prostate;
 CD82 antigen (R2 leukocyte antigen, antigen detected
 rc_AA086232_f_at AA086232 186 by monoclonal and antibody IA4)) 4.52 up 0.00452
 rc_AA086412_at AA086412 187 DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 16 3.13 up 0.00327
 AA089997_at AA089997 189 EST 4.9 up 0.0241
 AA091752_at AA091752 193 purine-rich element binding protein B 3.25 up 0.01419
 AA092129_f_at AA092129 194 EST 5.67 up 0.00011
 AA092290_f_at AA092290 195 EST 3.25 up 0.01616
 AA094752_at AA094752 203 hypothetical 43.2 Kd protein 3.44 up 0.04445
 rc_AA099404_s_at AA099404 208 EST 20.22 up 0
 rc_AA101272_at AA101272 215 EST 3.83 up 0.0386
 rc_AA102489_at AA102489 219 EST 5.28 up 0.02122
 rc_AA102837_f_at AA102837 221 EST 4.13 up 0.0067
 rc_AA112679_at AA112679 224 EST 4.19 up 0.00572
 rc_AA115562_at AA115562 229 EST 3.35 up 0.00283
 rc_AA115735_s_at AA115735 230 EST 4.8 up 0.02671
 rc_AA116036_at AA116036 233 chromosome 20 open reading frame 1 3.41 up 0.00089
 rc_AA122386_at AA122386 239 collagen, type v, alpha 2 3.44 up 0.02566
 rc_AA125808_at AA125808 240 EST 3.04 up 0.02112
 rc_AA127444_at AA127444 252 EST 3.87 up 0.01751
 rc_AA127741_at AA127741 256 EST 4.49 up 0.0463 Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_AA128407_at AA128407 259 EST 3.33 up 0.02298
 rc_AA129757_at AA129757 264 EST 3.75 up 0.0166
 rc_AA131220_at AA131220 267 EST 3.18 up 0.00974
 rc_AA132032_s_at AA132032 271 trinucleotide repeat containing 1 3.84 up 0.01136
 rc_AA132514_at AA132514 272 EST 3.2 up 0.00876
 rc_AA133527_at AA133527 281 EST 5.23 up 0.00037
 rc_AA133666_s_at AA133666 283 cysteine-rich protein 2 5.35 up 0.00433
 rc_AA134052_s_at AA134052 285 Rab geranylgeranyltransferase, alpha subunit 5.47 up 0.00982
 rc_AA135153_at AA135153 291 EST 5.58 up 0.00327
 rc_AA135871_at AA135871 294 EST 3.56 up 0.01718
 rc_AA136269_at AA136269 298 EST 7.5 up 0.00014

rc_AA136474_at AA136474 301 Meis (mouse) homolog 2 3.15 up 0.02837
 rc_AA136547_at AA136547 302 EST 4.19 up 0.00098
 rc_AA136864_at AA136864 304 zinc finger protein homologous to Zfp-36 in mouse 3.31 up 0.00346
 rc_AA142857_at AA142857 307 EST 9.48 up 0.00376
 rc_AA142858_at AA142858 308 EST 4.07 up 0.0022
 rc_AA146849_s_at AA146849 313 target of myb1 (chicken) homolog 4.72 up 0.00326
 rc_AA148885_at AA148885 320 minichromosome maintenance deficient (S. cerevisiae) 4 6.59 up 0.00112
 rc_AA148977_at AA148977 322 EST 9.3 up 0.00002
 rc_AA149889_at AA149889 326 neighbor of A-kinase anchoring protein 95 8.55 up 0.00224
 rc_AA151435_at AA151435 336 EST 4.52 up 0.01134
 ATP synthase, H⁺ transporting, mitochondrial F0
 rc_AA156187_at AA156187 339 complex, subunit b, isoform 1 9.38 up 0.02007
 rc_AA156460_at AA156460 343 EST 4.39 up 0.01223
 rc_AA159025_at AA159025 353 EST 6.58 up 0.01946
 rc_AA160775_s_at AA160775 355 BCL2-antagonist of cell death 3.8 up 0.01145
 3-prime-phosphoadenosine 5-prime-phosphosulfate
 rc_AA165526_at AA165526 360 synthase 1 3.68 up 0.00021
 rc_AA167708_at AA167708 363 EST 3.19 up 0.01871
 rc_AA171760_at AA171760 367 EST 4.39 up 0.04582
 rc_AA173430_at AA173430 371 EST 3.74 up 0.01159 Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 AA173505_at AA173505 372 EST 3 up 0.01736
 AA173597_at AA173597 373 EST 3.37 up 0.03622
 rc_AA173755_at AA173755 374 EST 6.73 up 0.00666
 rc_AA179787_at AA179787 380 polyglutamine binding protein 1 4.71 up 0.00725
 rc_AA179845_at AA179845 381 EST 3.55 up 0.02484
 rc_AA181580_s_at AA181580 383 karyopherin (importin) beta 1 3.01 up 0.0125
 rc_AA181705_f_at AA181705 385 EST 5.9 up 0.00023
 rc_AA182001_r_at AA182001 386 EST 3.78 up 0.04446
 AA187579_at AA187579 390 MCT-1 protein 3.4 up 0.02455
 rc_AA188378_i_at AA188378 392 EST 4.88 up 0.01653
 rc_AA194730_at AA194730 410 EST 4.57 up 0.00801
 rc_AA194998_at AA194998 413 purinergic receptor (family A group 5) 3.06 up 0.04752
 rc_AA195067_i_at AA195067 414 GTPase activating protein-like 3.24 up 0.00606
 rc_AA204927_at AA204927 425 tropomyosin 1 (alpha) 6.11 up 0.0014
 rc_AA207103_at AA207103 429 EST 3.36 up 0.00131
 rc_AA211483_at AA211483 435 EST 4.11 up 0.0365
 AA215299_s_at AA215299 439 U6 snRNA-associated Sm-like protein LSm7 4.81 up 0.00119
 rc_AA215379_at AA215379 440 EST 4.44 up 0.01675
 rc_AA218663_at AA218663 444 acid-inducible phosphoprotein 4.34 up 0.00161
 rc_AA226932_at AA226932 453 DKFZP564F0923 protein 5.25 up 0.00612
 rc_AA227145_at AA227145 454 EST 3.4 up 0.03422
 rc_AA227541_at AA227541 457 ns1-binding protein 3.6 up 0.02801
 AA232837_at AA232837 465 EST 8.85 up 0.0048
 rc_AA233897_at AA233897 476 EST 3.8 up 0.02145
 rc_AA234096_at AA234096 479 EST 5.75 up 0.01169
 rc_AA235289_at AA235289 495 RAP2A, member of RAS oncogene family 4.31 up 0.00135
 AA235448_s_at AA235448 497 EST 5.62 up 0.00077
 rc_AA235853_at AA235853 503 CGI-96 protein 3.16 up 0.00744
 rc_AA235868_at AA235868 504 nuclear transcription factor Y, beta 3.49 up 0.01897
 3-prime-phosphoadenosine 5-prime-phosphosulfate
 rc_AA236150_at AA236150 507 synthase 1 3.46 up 0.0008 Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 AA236412_at AA236412 511 EST 3.1 up 0.04463
 rc_AA236532_s_at AA236532 513 EST 3.04 up 0.03747
 rc_AA236672_at AA236672 515 EST 4.37 up 0.00385
 rc_AA236904_at AA236904 518 EST 3.07 up 0.01503
 rc_AA242757_at AA242757 522 EST 3.27 up 0.00286
 rc_AA243133_at AA243133 525 serine/threonine kinase 15 7.03 up 0.00005
 rc_AA243173_at AA243173 526 EST 3.49 up 0.0401
 AA249819_s_at AA249819 535 EST 5.22 up 0.00049
 rc_AA251230_at AA251230 540 EST 3.25 up 0.01417
 rc_AA251299_s_at AA251299 541 KIAA0014 gene product 4.74 up 0.0252
 rc_AA251428_at AA251428 542 DKFZP58612223 protein 3.15 up 0.01223
 rc_AA251766_at AA251766 543 EST 3.06 up 0.0098
 rc_AA251769_at AA251769 544 EST 4.45 up 0.01431
 rc_AA251792_at AA251792 546 fatty-acid-Coenzyme A ligase, long-chain 4 7.44 up 0.00285
 rc_AA251909_at AA251909

549 EST 3.59 up 0.01129
 rc_AA252060_at AA252060 550 EST 4.88 up 0.00169

 rc_AA252355_at AA252355 553 EST 3.02 up 0.00715
 rc_AA252524_at AA252524 555 EST
 3.17 up 0.00686
 chaperonin containing TCP1, subunit 6A (zeta 1), homeo

 rc_AA252627_s_at AA252627 556 box B5 4.28 up 0.00363
 rc_AA253011_f_at AA253011 558
 KIAA0713 protein 3.15 up 0.00035
 rc_AA255486_at AA255486 568 EST 3.72 up 0.00154

 rc_AA256131_at AA256131 574 glycerophosphatidylinositol anchor attachment 1 3.16 up 0.00011

 rc_AA256268_at AA256268 576 EST 3.13 up 0.03874
 rc_AA256524_at AA256524 580 AD022
 protein 3.06 up 0.00626
 rc_AA256606_at AA256606 581 EST 3.92 up 0.03087

 rc_AA256688_s_at AA256688 584 EST 4.23 up 0.03094
 rc_AA258131_at AA258131 587
 putative GTP-binding protein similar to RAY/RAB1C 6.23 up 0.00931
 rc_AA258182_at
 AA258182 589 EST 3.55 up 0.01198
 rc_AA258387_at AA258387 594 EST 3.15 up
 0.02028
 rc_AA258421_at AA258421 595 hypothetical protein 6.5 up 0.00559 Table 7B. Down
 regulated in hepatocellular carcinoma versus normal sample set 2.
 <P>Affy ID Genbank Seq ID
 Known Gene Name Fold Change Direction Pvalue
 rc_AA258614_s_at AA258614 599 EST 3.94
 up 0.0048
 rc_AA262477_at AA262477 608 ribonuclease HI, large subunit 4.57 up 0.00724

 rc_AA262957_at AA262957 612 EST 3.76 up 0.00157
 ATP synthase, H⁺ transporting,
 mitochondrial F0
 AA263032_s_at AA263032 614 complex, subunit b, isoform 1 6.73 up
 0.04478
 rc_AA278768_f_at AA278768 617 EST 3.77 up 0.03239
 rc_AA278817_at
 AA278817 618 EST 3.5 up 0.01159
 rc_AA279418_at AA279418 626 EST 3.23 up 0.02054

 rc_AA280734_i_at AA280734 639 KIAA0618 gene product 6.83 up 0.001
 rc_AA280840_at
 AA280840 641 casein kinase 1, gamma 2 4.51 up 0.0186
 rc_AA281599_at AA281599 647 EST
 4.87 up 0.00248
 rc_AA282247_at AA282247 657 EST 5.88 up 0.01112
 rc_AA282343_at
 AA282343 658 purine-rich element binding protein B 5.78 up 0.00128
 rc_AA282571_at
 AA282571 662 FSHD region gene 1 3.16 up 0.01355
 rc_AA283182_at AA283182 668 EST 6.78
 up 0.01784
 rc_AA283832_at AA283832 672 EST 4.77 up 0.00156
 rc_AA284565_f_at
 AA284565 675 EST 3.27 up 0.0362
 rc_AA284720_at AA284720 676 EST 3.03 up 0.00252

 rc_AA284945_at AA284945 680 EST 6.25 up 0.0002
 rc_AA285132_at AA285132 682 apoptotic
 protease activating factor 3.1 up 0.00844
 rc_AA286911_at AA286911 684 EST 3.36 up
 0.00037
 rc_AA291137_at AA291137 694 EST 3.67 up 0.03243
 rc_AA291139_at
 AA291139 695 EST 6.22 up 0.03491
 rc_AA291168_at AA291168 696 EST 4.93 up
 0.01633
 rc_AA291644_at AA291644 701 EST 3.28 up 0.00033
 rc_AA291659_at
 AA291659 702 EST 4.15 up 0.00019
 AA291786_s_at AA291786 704 FE65-LIKE 2 4.15 up
 0.00362
 rc_AA292765_at AA292765 712 ZW10 interactor 7.24 up 0.00498

 rc_AA292788_s_at AA292788 714 EST 3.65 up 0.01765
 rc_AA293420_s_at AA293420 717
 EST 4.05 up 0.01189
 rc_AA293589_s_at AA293589 719 zinc finger protein 3.02 up 0.01809
 Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.
 <P>Affy ID
 genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 AA293868_s_at AA293868
 721 EST 3.04 up 0.0054
 AA296994_s_at AA296994 724 seven transmembrane domain protein
 3.16 up 0.0076
 AA313213_at AA313213 732 flotillin 1 3.59 up 0.00878
 AA320369_s_at
 AA320369 735 chromosome 19 open reading frame 3 3.88 up 0.00452
 rc_AA321833_at
 AA321833 736 EST 3.16 up 0.00523
 rc_AA335191_f_at AA335191 741 creatine kinase, brain
 6.47 up 0.01462
 rc_AA338760_at AA338760 744 EST 3.96 up 0.01307
 rc_AA365708_s_at
 AA365708 764 microfibrillar-associated protein 1 3.01 up 0.02372
 AA365742_s_at AA365742
 765 tetraspan NET-6 protein 4.12 up 0.00255
 rc_AA370163_at AA370163 766 EST 3.41 up
 0.00134
 AA384184_s_at AA384184 774 DKFZP586B0519 protein 3.42 up 0.01222

 AA393139_at AA393139 775 geminin 7.44 up 0.008888
 rc_AA394258_s_at AA394258 779 RD
 RNA-binding protein 7.27 up 0.00054
 rc_AA398141_at AA398141 788 EST 3.3 up 0.0021

 rc_AA398205_at AA398205 789 EST 4.22 up 0.00059
 rc_AA398563_at AA398563 797 EST
 3.14 up 0.01895
 rc_AA398908_at AA398908 801 EST 20.72 up 0.00114

 rc_AA398926_f_at AA398926 802 EST 8.25 up 0.00066
 rc_AA399251_at AA399251 804 EST
 4.3 up 0.01578
 rc_AA399264_at AA399264 805 EST 3.51 up 0.00327
 rc_AA400184_at

AA400184 809 KIAA0907 protein 4.11 up 0.01123
 AA400643_s_at AA400643 817 GAS2-related on chromosome 22 4.04 up 0.03751
 rc_AA400896_at AA400896 822 EST 3.54 up 0.00889
 rc_AA401965_at AA401965 833 tumor suppressor deleted in oral cancer-related 1 7.58 up 0.00089
 rc_AA402272_at AA402272 837 EST 3.73 up 0.02336
 rc_AA402968_at AA402968 844 EST 3.68 up 0.00123
 O-linked N-acetylglucosamine (GlcNAc) transferase
 (UDP-N-acetylglucosamine:polypeptide-N-
 rc_AA40560_at AA40560 853 acetylglucosaminyl transferase) 3.73 up 0.0143
 rc_AA405098_at AA405098 855 EST 6.09 up 0.01224
 rc_Aa405505_at AA405505 860 RNA helicase family 4.05 up 0.007474 Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_AA405544_f_at AA405544 861 EST 3.09 up 0.04146
 rc_AA405791_at AA405791 864 EST 11.79 up 0.00587
 rc_AA406216_at AA406216 871 EST 3.4 up 0.00529
 rc_AA406384_at AA406384 875 KIAA0670 protein/acinus 3.23 up 0.00486
 rc_AA410469_at AA410469 883 EST 5.45 up 0.00068
 rc_AA410962_s_at AA410962 887 peroxisome proliferative activated receptor, delta 4.91 up 0.0044
 rc_AA412301_at AA412301 899 eST 3.42 up 0.0129
 rc_AA412720_at AA412720 905 EST 3.06 up 0.02153
 rc_AA416970_at AA416970 912 Mad4 homology 5.3 up 0.00418
 rc_AA416973_at AA416973 913 EST 4.29 up 0.00155
 rc_AA417030_at AA417030 914 EST 7.35 up 0.00555
 rc_AA417884_at AA417884 919 cyclin-dependent kinase inhibitor 2C (p18,inhibitin 3.42 up 0.02997
 AA421213_at AA421213 931 Lsm3 protein 3.34 up 0.00198
 rc_AA421562_at AA421562 934 anterior gradient 2 (Xenopus laevis) homolog 5.02 up 0.02818
 rc_AA421951_at AA421951 936 EST 6.69 up 0.00013
 rc_AA423827_f_at AA423827 941 chromosome 22 open reading frame 3 4.39 up 0.00345
 rc_AA423841_f_at AA423841 942 EST 3.71 up 0.01481
 rc_AA424029_at AA424029 943 EST 4.54 up 0.02721
 rc_AA424487_at AA424487 945 EST 4.68 up 0.0013
 rc_AA424881_at AA424881 949 EST 3.39 up 0.03546
 eukaryotic translation initiation factor 2B, subunit 2 (beta,
 rc_AA425544_s_at AA425544 955 39kD) 3.05 up 0.0346
 rc_AA425852_at AA425852 958 EST 3.98 up 0.02796
 rc_AA425852_i_at AA425852 958 EST 3.82 up 0.0395
 rc_AA426291_at AA426291 961 EST 3.03 up 0.00365
 rc_AA426374_f_at AA426374 964 tubulin, alpha 2 3.25 up 0.04346
 rc_AA426447_at AA426447 965 EST 3.01 up 0.02414
 rc_AA426521_at AA426521 967 Sjogren's syndrome nuclear autoantigen 1 3.33 up 0.01163
 rc_AA427734_at AA427734 977 cholinergic receptor, nicotinic, epsilon polypeptide 3.08 up 0.04796
 AA428172_f_at AA428172 986 Notch (Drosophila) homolog 3 9.63 up 0.00195 Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene name Fold Change Direction Pvalue
 rc_AA428204_at AA428204 987 subunit 6 (77kD) 3.08 up 0.00313
 rc_AA429470_at AA429470 996 EST 3.2 up 0.0153
 rc_AA429472_at AA429472 997 DKFZP434P106 protein 8.78 up 0.00063
 rc_AA429539_f_at AA429539 999 EST 4.3 up 0.01035
 rc_AA429572_at AA429572 1000 ribosomal protein S6 3.31 up 0.02144
 rc_AA429825_at AA429825 1003 DKFZP566B023 protein 3.11 up 0.01857
 rc_AA430032_at AA430032 1009 pituitary tumor-transforming 1 10.67 up 0.00052
 rc_AA43048_at AA43048 1012 KIAA0160 protein 4.32 up 0.00279
 rc_AA430154_at AA430154 1014 EST 3.09 up 0.04401
 rc_AA430474_at AA430474 1015 EST 4.69 up 0.00007
 rc_AA430675_at AA430675 1019 Fanconi anemia, complementation group G 3.16 up 0.01007
 rc_AA431571_at AA431571 1024 EST 4.62 up 0.0174
 rc_AA431719_at AA431719 1025 EST 3.19 up 0.00294
 rc_AA433947_at AA433947 1034 EST 3.09 up 0.00253
 rc_AA434418_at AA434418 1036 KIAA1115 protein 6.75 up 0.0032
 rc_AA435662_f_at AA435662 1039 EST 3.27 up 0.0433
 rc_AA435665_at AA435665 1040 EST 3.94 up 0.00274
 rc_AA435681_s_at AA435681 1041 EST 3.07 up 0.01166
 rc_AA435748_at AA435748 1044 EST 5.01 up 0.01812
 rc_aa435769_s_at AA435769 1046 EST 3.06 up 0.00615
 rc_AA442054_s_at AA442054 1067 phospholipase C, gamma 1 (formerly subtype 148) 4.94 up 0.04102
 rc_AA442155_at AA442155 1068 transforming acidic coiled-coil containing protein 3 3.35 up 0.00344
 rc_AA442400_at AA442400 1071 hepatitis B virus x-

interacting protein (9.6kD) 3.02 up 0.04037
 rc_AA442763_at AA442763 1072 cyclin B2 3.49 up 0.04176
 rc_AA443271_at AA443271 1073 KIAA0546 protein 3.44 up 0.00324
 rc_AA443316_s_at AA443316 1075 v-Ha-ras Harvey rat sarcoma viral oncogene homolog 3.4 up 0.00133
 rc_AA443602_at AA443602 1078 EST 5.71 up 0.00736
 rc_AA443802_at AA443802 1081 EST 4.07 up 0.01546
 rc_AA446242_at AA446242 1087 EST 6.3 up 0.00169
 rc_AA446570_at AA446570 1089 EST 3.12 up 0.02228 Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_AA446581_at AA446581 1090 DKFZP564P0462 protein 4.04 up 0.00479
 rc_AA446970_at AA446970 1098 EST 3.09 up 0.01627
 rc_AA447574_at AA447574 1102 EST 4.12 up 0.00779
 rc_AA448252_at AA448252 1114 EST 3 up 0.00256
 rc_aa449073_s_at AA449073 1117 EST 5.61 up 0.01214
 rc_aa449431_s_at AA449431 1124 translation initiation factor IF2 3.76 up 0.00571
 rc_AA449828_at AA449828 1130 EST 3.35 up 0.01609
 rc_AA450247_at AA450247 1133 EST 3.13 up 0.00531
 hepatocellular carcinoma associated protein; breast
 rc_AA451680_at AA451680 1136 cancer associated gene 1 3.85 up 0.0018
 rc_AA451877_at AA451877 1138 EST 4.6 up 0.04045
 AA451992_at AA451992 1140 HSPC039 protein 3.33 up 0.01696
 rc_AA452167_at AA452167 1142 EST 3.29 up 0.03337
 AA452724_at AA452724 1149 programmed cell death 5 7.7 up 0.00085
 rc_AA453628_at AA453628 1154 EST 3.17 up 0.00849
 rc_AA453656_at AA453656 1155 EST 3.02 up 0.00958
 rc_AA453783_s_at AA453783 1158 EST 4.07 up 0.00786
 rc_AA454597_s_at AA454597 1166 EST 4.23 up 0.00917
 rc_AA454830_at AA454830 1170 DKFZP586M2123 protein 6.48 up 0.00555
 AA454908_s_at AA454908 1171 KIAA0144 gene product 6.39 up 0.01835
 rc_AA455239_at AA455239 1174 chromosome-associated polypeptide C 5.78 up 0.00003
 rc_AA456415_at AA456415 1192 KIAA0537 gene product 3.32 up 0.00155
 rc_AA456583_s_at AA456583 1193 PL6 protein 3.37 up 0.00139
 rc_AA456646_at AA456646 1196 EST 3.34 up 0.0309
 rc_AA456852_at AA456852 1199 supressor of white apricot homolog 2 3.66 up 0.00614
 rc_AA458878_s_at AA458878 1204 EST 5.49 up 0.00977
 rc_AA458890_at AA458890 1206 EST 3.27 up 0.00079
 rc_AA459254_at AA459254 1211 EST 6.22 up 0.00001
 rc_AA459542_s_at AA459542 1218 regulatory factor X-associated ankyrin-containing protein 3.4 up 0.00841
 rc_AA460665_at AA460665 1230 EST 4.01 up 0.01866
 rc_aa460909_s_at AA460909 1232 EST 5.02 up 0.01354 Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_AA461063_at AA461063 1235 EST 4.3 up 0.00074
 AA461282_s_at AA461282 1237 dihydropyrimidinase-like 2 3.42 up 0.02014
 rc_AA461476_at AA461476 1243 EST 3.72 up 0.00744
 rc_AA463254_s_at AA463254 1247 histone deacetylase 3 4.01 up 0.01856
 rc_AA463934_at AA463934 1253 splicing factor 3b, subunit 4, 49kD 3.15 up 0.00592
 rc_AA464043_s_at AA464043 1255 EST 3.99 up 0.00056
 rc_AA464251_s_at AA464251 1257 EST 3.45 up 0.02229
 rc_AA464414_i_at AA464414 1258 EST 4.08 up 0.02299
 rc_AA464423_at AA464423 1259 EST 3.06 up 0.01416
 rc_aa464722_s_at AA464722 1263 KFZP566C243 protein 3.51 up 0.00101
 rc_AA464963_at AA464963 1265 EST 4.77 up 0.00086
 AA465000_s_at AA465000 1266 EST 3.86 up 0.00431
 rc_AA465093_at AA465093 1267 TIA1 cytotoxic granule-associated RNA-binding protein 3.3 up 0.01314
 rc_AA465218_at AA465218 1268 DKFP586M1523 protein 3.17 up 0.00357
 rc_AA465342_at AA465342 1271 EST 3.21 up 0.01378
 rc_AA470156_at AA470156 1276 EST 4.99 up 0.0206
 AA471384_at AA471384 1278 divalent cation tolerant protein CUTA 3.44 up 0.01161
 rc_AA476473_at AA476473 1285 EST 3 up 0.01324
 rc_AA476754_s_at AA476754 1287 EST 3.18 up 0.01696
 rc_AA476944_at AA476944 1288 EST 3.29 up 0.00189
 rc_AA477316_at AA477316 1290 calcumenin 3.05 up 0.00608
 rc_AA477549_s_at AA477549 1291 T-cell, immune regulator 1 4.84 up 0.04906
 rc_AA478017_at AA478017 1295 zyxin 4.25 up 0.01223
 rc_AA478300_at AA478300 1298 CD39-like 2 3.75 up 0.00152
 rc_AA478415_at AA478415 1299 EST 3.14 up 0.0483
 rc_AA478422_at AA478422 1301 unc-51 (C. elegans)-like kinase 1 3.83 up 0.00116

rc_AA478615_s_at AA478615 1305 H1 histone family, member X 3.09 up 0.0499
 disabled (Drosophila) homolog 2 (mitogen-responsive
 rc_AA478971_s_at AA478971 1306 phosphoprotein) 3.25 up 0.02698
 rc_AA479096_at AA479096 1308 EST 3.32 up 0.00118
 rc_AA479139_s_at AA479139 1310 acid phosphatase 1, soluble 3.42 up 0.01853 Table 7B. Down Regulated in hepatocellular carcinoma versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_AA47988_at AA479881 1317 EST 3.34 up 0.3289
 rc_AA481060_at AA481060 1326 EST 3.08 up 0.00029
 rc_AA481420_at AA481420 1327 EST 3.08 up 0.0206
 rc_AA482104_s_at AA482104 1332 no-metastatic cells 3, protein expressed in 4.78 up 0.00135
 rc_AA482224_f_at AA482224 1334 putative type II membrane protein 4.47 up 0.0001
 AA482319_f_at AA482319 1335 putative type II membrane protein 4.9 up 0.00028
 AA482319_i_at AA482319 1335 putative type II membrane protein 3.13 up 0.00071
 rc_AA485060_at AA485060 1339 EST 3.83 up 0.03172
 rc_AA485084_s_at AA485084 1340 EST 3.31 up 0.01232
 rc_AA485431_s_at AA485431 1345 EST 3.81 up 0.00441
 rc_AA485697_at AA485697 1346 EST 3.53 up 0.03566
 rc_AA487218_at AA487218 1355 EST 4.43 up 0.03198
 rc_AA487856_at AA487856 1359 KIAA0676 protein 3.59 up 0.1408
 rc_AA48807_at AA488074 1360 cell division cycle 42 (GTP-binding protein, 25kD) 3.74 up 0.01887
 rc_AA88432_at AA48432 1361 phosphoserine phosphatase 4.2 up 0.00128
 rc_AA88872_s_at AA488872 1363 EST 3.35 up 0.03191
 rc_AA488892_at AA488892 1364 EST 4.14 up 0.04766
 rc_AA489091_at AA489091 1368 EST 3.58 up 0.0002
 rc_AA489707_at AA489707 1371 EST 3.5 up 0.03208
 rc_AA489712_at AA489712 1372 EST 4.69 up 0.00587
 rc_AA490212_at AA490212 1375 H2A histone family, member Y 3.52 up 0.02202
 solute carrier family 2 (facilitated glucose transporter),
 AA491188_at AA491188 1387 member 3 5.04 up 0.02291
 rc_AA491295_at AA491295 1390 calcium/calmodulin-dependent protein kinase kinase 2, 3.71 up 0.0103
 AA495857_at AA495857 1394 EST 3.21 up 0.02243
 rc_AA496715_f_at AA496715 1400 spectrin SH3 domain binding protein 1 3.44 up 0.00069
 v-erb-b2 avian erythroblastic leukemia viral oncogene
 rc_AA496981_at AA496981 1404 homolog 3 5.82 up 0.00521
 rc_AA497018_at AA497018 1406 adenylate cyclase 1 (brain) 4.81 up 0.00352
 AA054413_at AA504413 1413 EST 3.31 up 0.00036
 rc_AA504512_s_at AA504512 1415 KIAA0943 protein 5.72 up 0.00384 Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 solute carrier family 2 (facilitated glucose transporter),
 rc_AA505133_at AA505133 1417 member 3 12.21 up 0.00169
 rc_AA505141_at AA505141 1418 EST 3.08 up 0.02327
 rc_AA521149_at AA521149 1420 EST 3.33 up 0.00211
 rc_AA598405_at AA598405 1424 membrane interacting protein of RGS16 3.87 up 0.00649
 rc_AA598447_at AA598447 1428 exportin, tRNA (nuclear export receptor for tRNAs) 3.5 up 0.01201
 rc_AA598589_at AA598589 1431 EST 3.24 up 0.00432
 SWI/SNF related, matrix associated, actin dependent
 rc_AA598648_s_at AA598648 1432 regulator of chromatin, subfamily a, member 4 3.46 up 0.00293
 rc_AA598712_at AA598712 1436 EST 3.45 up 0.00005
 rc_AA598749_at AA598749 1438 EST 3.01 up 0.03714
 heterogeneous nuclear ribonucleoprotein U (scaffold
 rc_AA598829_s_at AA598829 1439 attachment factor A) 3.04 up 0.00967
 rc_AA598831_f_at AA598831 1440 EST 3.41 up 0.00452
 rc_AA599469_at AA599469 1450 EST 3.07 up 0.04154
 rc_AA599808_at AA599808 1455 EST 3.09 up 0.00726
 rc_AA599850_at AA599850 1457 EST 3.55 up 0.03215
 rc_AA600153_at AA60153 1460 DEK oncogene (DNA binding) 3.71 up 0.02967
 rc_AA608668_at AA608668 1465 erythrocyte membrane protein band 4.1-like 2 3.33 up 0.02014
 rc_AA608897_at AA608897 1473 EST 5.05 up 0.01782
 rc_AA609008_at AA609008 1475 EST 4.04 up 0.00002
 rc_AA609080_at AA609080 1478 EST 3.71 up 0.0306
 rc_AA610073_at AA610073 1497 EST 3.25 up 0.00859
 rc_AA610089_at AA610089 1498 U4/U6-associated RNA splicing factor 4.07 up 0.00361
 rc_AA610116_i_at AA610116 1499 tetraspan NET-6 protein 16.35 up 0.00249
 rc_AA620461_at AA620461 1501 EST 3.45 up 0.01146
 rc_AA620553_s_at AA620553 1504 flap structure-specific endonuclease 1 7.56 up 0.00101
 rc_AA620761_at AA620761 1507 EST 3.3 up

0.00285
 rc_AA620779_at AA620779 1508 golgin-67 3.35 up 0.00297
 rc_AA620881_at AA620881 1510 trinucleotide repeat containing 3 9.49 up 0.00062
 rc_AA621146_at AA621146 1514 MUF1 protein 3.15 up 0.02116 table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_AA621242_s_at AA621242 1518 hypothetical protein,peptidylprolyl isomerase B 4.59 up 0.00081
 rc_AA621367_at AA621367 1523 EST 3.1 up 0.00066
 rc_AA621409_at AA621409 1524 putative type II membrane protein 3.5 up 0.00462
 rc_AA621530_at AA621530 1526 EST 3.26 up 0.00298
 rc_AA621535_at AA621535 1527 FE65-LIKE 2 3.37 up 0.0167
 rc_AA621752_at AA621752 1529 26S proteasome-associated pad1 homolog 3.13 up 0.01571
 AB002373_at AB002373 1538 KIAA0375 gene product 4.41 up 0.00795
 AF003521_at AF003521 1545 jagged 2 3.58 up 0.00299
 AF004022_at AF004022 1546 serine/threonine kinase 12 3.29 up 0.00841
 C00358_at C00358 1552 nucleolar protein 3 (apoptosis repressor with CARD 3.45 up 0.00985
 C01721_at C01721 1558 phospholipase C, beta 3, neighbor pseudogene 5.89 up 0.0383
 C01766_s_at C01766 1559 EST 8.18 up 0.00505
 rc_C14051_f_at C14051 1565 phosphorprotein enriched in astrocytes 15 4.79 up 0.00548
 rc_C14098_f_at C14098 1566 EST 4.62 up 0.01654
 rc_C14756_f_at C14756 1570 MLN51 protein 3.75 up 0.0226
 rc_C14835_f_at C14835 1571 EST 3.35 up 0.0316
 D00596_at D00596 1590 thymidylate synthetase 5.58 up 0.0098
 D13370_at D13370 1603 APEx nuclease (multifunctional DNA repair enzyme) 3.07 up 0.00857
 general transcription factor IIIC, polypeptide 2 (beta
 D13636_at D13636 1606 subunit, 110kD) 3.12 up 0.00022
 D13640_at D13640 1608 KIAA0015 gene product 3.55 up 0.00347
 D14657_at D14657 1615 KIAA0101 gene product 3.84 up 0.02048
 rc_D20899_at D20899 1626 EST 3.13 up 0.02128
 minichromosome maintenance deficient (S. cerevisiae) 2
 D21063_at D21063 1628 (mitotin) 3.25 up 0.03558
 D26129_at D26129 1635 ribonuclease, RNase A family, 1 (pancreatic) 6.9 up 0.00008
 D28589_at D28589 1637 EST 3.38 up 0.01144
 D30946_at D30946 1638 kinesin family member 3B 3.43 up 0.01458
 D31094_at D31094 1639 G8 protein 9.37 up 0.0048
 D31294_at D31294 1643 EST 3.3 up 0.004
 D31417_at D31417 1645 secreted protein of unknown function 3.69 up 0.0004 Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 D38073_at D38073 1651 minichromosome maintenance deficient (S. cerevisiae) 3 4.1 up 0.01195
 D38305_at D38305 1652 transducer of ERBB2, 1 3.22 up 0.0215
 D42040_s_at D42040 1657 female sterile homeotic-related gene 1 (mouse homolog) 4.02 up 0.00389
 rc_D51072_s_at D51072 1674 biliverdin reductase A 3.34 up 0.0254
 rc_D51276_f_at D51276 1678 leukemia-associated phosphoprotein p18 (stathmin) 9.42 up 0.00015
 D55716_at D55716 1686 minichromosome maintenance deficient (S. cerevisiae) 7 5.48 up 0.00003
 rc_D57317_at D57317 1688 activated RNA polymerase II transcription cofactor 4 3.17 up 0.00464
 rc_D59355_s_at D59355 1696 cytoskeleton-associated protein 1 6.05 up 0.0015
 rc_D59553_f_at D59553 1697 golgin-67 5.95 up 0.00169
 rc_D59570_f_at D59570 1699 EST 4.34 up 0.00487
 rc_D60811_s_at D60811 1704 EST 4.34 up 0.00217
 D63478_at D63478 1711 KIAA0144 gene product 3.89 up 0.00253
 D63486_at D63486 1712 KIAA0152 gene product 3.56 up 0.00063
 rc_D80420_at D80420 1732 ubiquinol-cytochrome c reductase hinge protein 3.86 up 0.00412
 rc_D80710_f_at D80710 1734 integral type I protein 3.17 up 0.04549
 rc_D80917_f_at D80917 1736 KIAA0670 protein/acinus 3.09 up 0.00168
 rc_D80946_f_at D80946 1737 SFRS protein kinase 1 3.07 up 0.00986
 D81608_at D81608 1740 polymerase (RNA) II (DNA directed) polypeptide K 3.52 up 0.00437
 D82226_s_at D82226 1742 proteasome (prosome, macropain) 26S subunit, 4.35 up 0.00184
 D82277_s_at D82277 1743 LDL induced EC protein 3.33 up 0.00355
 D82558_at D82558 1746 novel centrosomal protein RanBPM 4.67 up 0.00458
 trinucleotide repeat containing 11 (THR-associated
 D83783_at D83783 1748 protein, 230 kDa subunit) 4.16 up 0.00055
 D84557_at D84557 1749 minichromosome maintenance deficient (mis5, S. 3.97 up 0.0017
 D86957_at D86957 1754 KIAA0202 protein 3.08 up 0.02949
 D86977_at D86977 1757 KIAA0224 gene product 3.03 up 0.00053
 rc_F01538_s_at F01538 1771 RAP1, GTPase activating protein 1 4.88

up 0.00292
 rc_F01568_at F01568 1772 EST 4.13 up 0.00084
 rc_F01831_at F01831 1773 EST 5.95 up 0.00532
 rc_F02254_s_at F02254 1777 Fas-activated serine/threonine kinase 5.1 up 0.00329
 rc_F02807_at F02807 1781 KIAA0838 protein 5.67 up 0.02064 Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_F02863_at F02863 1782 EST 3.05 up 0.03504
 rc_F04320_s_at F04320 1786 replication factor C (activator 1) 4 (37kD) 6.29 up 0.00042
 rc_F04444_at F04444 1788 EST 4.13 up 0.00944
 rc_F04479_at F04479 1789 KIAA1067 protein 3.23 up 0.04522
 rc_F08876_at F08876 1797 EST 9.06 up 0
 procollagen-proline, 2-oxoglutarate 4-dioxygenase
 rc_F09788_at F09788 1808 (proline 4-hydroxylase), alpha polypeptide II 3.67 up 0.01682
 rc_F10199_f_at F10199 1813 EST 3.93 up 0.03209
 rc_F10290_at F10290 1815 EST 3.39 up 0.02392
 rc_F10453_at F10453 1819 EST 3.64 up 0.01878
 rc_F10741_at F10741 1822 KIAA0622 protein 3.01 up 0.03079
 rc_F13809_f_at F13809 1828 tropomyosin 1 (alpha) 4.4 up 0.01221
 rc_H00540_at H00540 1829 EST 3.74 up 0.00234
 rc_H05084_at H05084 1844 EST 5.85 up 0.0059
 rc_H07873_at H07873 1856 EST 3.53 up 0.0391
 rc_H08863_at H08863 1859 hypothetical protein 7.18 up 0.02102
 rc_H09241_s_at H09241 1861 EST 3.05 up 0.01487
 rc_H09271_f_at H09271 1862 EST 4.78 up 0.00072
 rc_H10933_at H10933 1873 EST 6.18 up 0.00003
 rc_H11320_s_at H11320 1875 SUMO-1 activating enzyme subunit 2 3.06 up 0.00167
 rc_H16251_s_at H16251 1886 EST 3.3 up 0.03286
 rc_H27188_f_at H27188 1908 collagen-binding protein 2 (collagen 2) 5.84 up 0.01826
 rc_H27897_s_at H27897 1911 hypothetical protein 3.01 up 0.00174
 rc_H28333_f_at H28333 1912 melanoma adhesion molecule 4.94 up 0.00166
 rc_H41529_at H41529 1926 EST 5.06 up 0.03309
 H46486_s_at H46486 1932 nesca protein 4.57 up 0.00749
 rc_H47357_f_at H47357 1934 EST 3.65 up 0.03799
 rc_H48459_s_at H48459 1937 KIAA0186 gene product 3.1 up 0.02325
 rc_H52937_at H52937 1944 roundabout (axon guidance receptor, Drosophila) 4.02 up 0.00163
 rc_H56345_r_at H56345 1950 EST 3.73 up 0.00853
 rc_H57709_s_at H57709 1956 ribosomal protein L31 4.41 up 0.00091 Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_H59617_at H59617 1964 EST 5.81 up 0.0115
 rc_H62474_f_at H62474 1970 EST 3.39 up 0.04173
 rc_H64493_f_at H64493 1973 immunoglobulin heavy constant gamma 3 (G3m marker) 4.74 up 0.00751
 phospholipase A2, group VII (platelet-activating factor
 rc_H65030_s_at H65030 1974 acetylhydrolase, plasma) 3.26 up 0.02278
 rc_H65042_at H65042 1975 EST 3.44 up 0.0006
 H67964_at H67964 1981 EST 3.06 up 0.02707
 rc_H68794_at H68794 1984 EST 3.67 up 0.00327
 rc_H70739_f_at H70739 1991 EST 4.34 up 0.00106
 rc_H73484_s_at H73484 1995 ferritin, heavy polypeptide 1 3.18 up 0.00432
 rc_H78211_at H78211 2001 EST 7.5 up 0.02674
 rc_H86072_f_at H86072 2015 EST 4.49 up 0.01301
 rc_H88674_s_at H88674 2021 collagen, type I, alpha 2 4.15 up 0.02664
 rc_H89987_s_at H89987 2027 ATP-binding cassette, sub-family C (CFTR/MRP), 3.13 up 0.01194
 rc_H91632_at H91632 2031 EST 3.5 up 0.03688
 rc_H94471_at H94471 2042 occludin 6.26 up 0.00379
 rc_H96850_at H96850 2055 dolichyl-diphosphooligosaccharide-protein 3.03 up 0.00679
 rc_H97012_at H97012 2058 EST 3.51 up 0.03505
 rc_H97013_at H97013 2059 ephrin-A4 6.8 up 0.00023
 rc_H97677_s_at H97677 2062 EST 4.34 up 0.00753
 rc_H99261_s_at H99261 2074 EST 3.33 up 0.00319
 rc_H99364_at H99364 2075 chloride channel 7 3.03 up 0.01727
 rc_H99473_s_at H99473 2077 regulator of nonsense transcripts 1 6.51 up 0.00025
 rc_H99489_s_at H99489 2078 quiescin Q6 3.4 up 0.02682
 rc_H99587_s_at H99587 2079 EST 4.44 up 0.00532
 rc_H99774_at H99774 2081 EST 3.51 up 0.00009
 rc_H99877_at H99877 2083 exportin, tRNA (nuclear export receptor for tRNAs) 3.75 up 0.00302
 rc_H99879_at H99879 2084 EST 10.81 up 0.001 Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 J00231_f_at J00231 2087 immunoglobulin heavy constant gamma 3 (G3m marker) 6.23 up 0.00177
 J03040_at J03040 2091 secreted protein, acidic, cysteine-rich (osteonectin) 3.77 up 0.00594
 J03464_s_at J03464 2094 collagen, type I, alpha 2 10.37 up

0.00979
 keratin 10 (epidermolytic hyperkeratosis; keratosis
 J04029_s_at J04029 2102 palmaris et plantaris) 3.02 up 0.00032
 J05614_at J05614 2122 EST 3.73 up 0.03419
 L03411_s_at L03411 2134 RD RNA-binding protein 4.06 up 0.00467
 L04270_at L04270 2135 lymphotoxin beta receptor (TNFR superfamily, member 3.5 up 0.01547
 L06797_s_at L06797 2143 chemokine (C-X-C motif), receptor 4 (fusin) 3.23 up 0.04782
 L11669_at L11669 2157 tetracycline transporter-like protein 3.4 up 0.02062
 high-mobility group (nonhistone chromosomal) protein
 L17131_ma1_at L17131 2168 isoforms I and Y 4.45 up 0.03141
 TATA box binding protein (TBP)-associated factor, RNA
 L25444_at L25444 2181 polymerase II, E, 70/85kD 3.78 up 0.00011
 cyclin-dependent kinase inhibitor 3 (CDK2-associated
 L25876_at L25876 2182 dual specificity phosphatase) 4.43 up 0.00082
 L28821_at L28821 2188 mannosidase, alpha, class 2A, member 2 4.63 up 0.00876
 L29218_s_at L29218 2190 CDC-like kinase 2 6.51 up 0.00019
 L29218_at L29218 2190 CDC-like kinase 2 3.82 up 0.00035
 L33930_s_at L33930 2198 CD24 antigen (small cell lung carcinoma cluster 4 4.35 up 0.3968
 transcription elongation factor B (SIII), polypeptide 1
 L34587_at L34587 2200 (15kD, elongin C) 3.12 up 0.00946
 L47125_s_at L47125 2218 glypican 3 10.69 up 0.04129
 L76191_at L76191 2222 interleukin-1 receptor-associated kinase 1 3.85 up 0.00152
 excision repair cross-complementing rodent repair
 L76568_xpt3_f_at L76568 2225 deficiency, complementation group 4 3.4 up 0.0172
 M12125_at M12125 2241 tropomyosin 2 (beta) 7.13 up 0.0004
 M14483_ma1_s_at M14483 2261 prothymosin, alpha (gene sequence 28) 3.36 up 0.00033
 M19267_s_at M19267 2286 tropomyosin 1 (alpha) 4.3 up 0.00893 Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 M21259_at M21259 2293 small nuclear ribonucleoprotein polypeptide E 3.68 up 0.00415
 M26576_cds2_at M26576 2310 EST 3.48 up 0.00062
 AFF-M27830_5_at M27830 2314 EST 4.6 up 0.04719
 AFF-M27830_M_at M27830 2314 EST 3.54 up 0.00777
 AFF-M27830_5_at M27830 2314 EST 3.3 up 0.02453
 M31303_ma1_at M31303 2327 leukemia-associated phosphoprotein p18 (stathmin) 5.86 up 0.00071
 M32977_s_at M32977 2336 vascular endothelial growth factor 3.93 up 0.04917
 v-erb-b2 avian erythroblastic leukemia viral oncogene
 M34309_at M34309 2342 homolog 3 3.49 up 0.00191
 M35252_at M35252 2343 transmembrane 4 superfamily member 3 4.65 up 0.04128
 M37583_at M37583 2349 H2A histone family, member Z 4.25 up 0.00135
 M55210_at M55210 2353 laminin, gamma 1 (formerly LAMB2) 3.47 up 0.02551
 M55998_s_at M55998 2356 collagen, type I, alpha 1 3.54 up 0.01449
 M57710_at M57710 2357 lecti, galactoside-binding, soluble, 3 (galectin 3) 6.76 up 0.00103
 M57730_at M57730 2358 ephrin-A1 3.39 up 0.00199
 M60784_s_at M60784 2368 small nuclear ribonucleoprotein polypeptide A 4.74 up 0.00001
 M61916_at M61916 2372 laminin, beta 1 3.18 up 0.01171
 M63573_at M63573 2377 peptidylprolyl isomerase B (cyclophilin B) 3.59 up 0.00916
 M68864_at M68864 2389 ORF 3.95 up 0.00144
 M86667_at M86667 2411 nucleosome assembly protein 1-like 1 3.08 up 0.00473
 stress-induced-phosphoprotein 1 (Hsp70/Hsp90-
 M86752_at M86752 2412 organizing protein) 5.15 up 0.02881
 M87339_at M87339 2415 replication factor C (activator 1) 4 (37kD) 4.59 up 0.00116
 M91083_at M91083 2419 chromosome 11 open reading frame 13 3.19 up 0.00243
 membrane component, chromosomal 4, surface marker
 M93036_at M93036 2422 (35kD glycoprotein) 3.07 up 0.04199
 M94250_at M94250 2426 midkine (neurite growth-promoting factor 2) 9.86 up 0.02104
 M94345_at M94345 2427 capping protein (actin filament), gelsolin-like 3.59 up 0.04508
 M97856_at M97856 2436 nuclear autoantigenic sperm protein (histone-binding) 3.21 up 0.00444
 rc_N21407_at N21407 2443 EST 3.47 up 0.01037
 rc_N21648_s_at N21648 2447 MpV17 transgene, murine homolog, glomerulosclerosis 3.73 up 0.00071 Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_N26904_at N26904 2469 EST 15.38 up 0.00077
 rc_N29484_at N29484 2478 EST 3.08 up 0.04834
 rc_N29742_at N29742 2481 EST 3.74 up 0.00104
 rc_N31597_s_at N31597 2487 DKFZP564G2022 protein 3.17 up 0.03017
 rc_N33920_at N33920 2493 diubiquitin 50.29 up 0
 rc_N34825_s_at N34825 2498

DKFZP434P106 protein 3.27 up 0.01334
 rc_N35913_at N35913 2503 EST 3.48 up 0.0016
 rc_N36432_at N36432 2507 erythrocyte membrane protein band 4.1-like 2 7.95 up 0.00067
 rc_N29237_at N29237 2511 EST 3.45 up 0.02481
 N42272_s_at N42272 2515 EST 3.03 up 0.0017
 eukaryotic translation initiation factor 3, subunit 3
 rc_N47956_at N47956 2524 (gama, 40kD) 3.76 up 0.00968
 rc_N48790_at N48790 2532 EST 3.32 up 0.00654
 rc_N51590_s_at N51590 2546 EST 3.01 up 0.04345
 rc_N51771_at N51771 2548 KIAA0652 gene product 3.5 up 0.00028
 ADP-ribosyltransferase (NAD⁺; poly (ADP-ribose)
 rc_N51855_at N51855 2550 polymerase)-like 3 3.39 up 0.00115
 rc_N52168_at N52168 2551 EST 3.66 up 0.00127
 rc_N53067_at N53067 25507 DKFZP547E1010 protein 3.1 up 0.00101
 rc_N54067_at N54067 2562 mitogen-activated protein kinase kinase kinase 4 4.82 up 0.00229
 rc_N54841_at N54841 2572 EST 5.87 up 0.02752
 rc_N56935_s_at N56935 2575 EST 4.04 up 0.00797
 rc_N59536_at N59536 2586 EST 11.68 up 0.00484
 rc_N62126_at N62126 2589 EST 6.42 up 0.00109
 rc_N64374_at N64374 2608 KIAA0537 gene product 3.25 up 0.01652
 rc_N67815_f_at N67815 2627 EST 3.84 up 0.00439
 rc_N68018_at N68018 2631 TBP-associated factor 172 3.84 up 0.00277
 rc_N68241_at N68241 2634 EST 4.32 up 0.00532
 rc_N69084_i_at N69084 2643 EST 3.11 up 0.0094
 rc_N69252_f_at N69252 2647 ferritin, light polypeptide 3.69 up 0.04116
 rc_N69263_at N69263 2648 EST 5.26 up 0.0276 Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_N69390_at N69390 2650 EST 3.99 up 0.00016
 rc_N69879_s_at N69879 2651 drebrin 1 3.15 up 0.01659
 rc_N70481_at N70481 2658 EST 4.13 up 0.0099
 rc_N70678_s_at N70678 2660 TAR (HIV) RNA-binding protein 1 3.78 up 0.02858
 solute carrier family 11 (proton-coupled divalent metal
 rc_N72116_s_at N72116 2668 ion transporters), members 2 5.57 up 0.00709
 rc_N73705_at N73705 2677 EST 3.75 up 0.01762
 rc_N73762_f_at N73762 2678 EST 3.67 up 0.00796
 rc_N73808_f_at N73808 2679 EST 6.44 up 0.00352
 rc_N73865_at N73865 2681 EST 4.43 up 0.00177
 rc_N75541_at N75541 2692 EST 4.43 up 0.01059
 rc_N80703_at N80703 2704 EST 5.65 up 0.0001
 rc_N90238_i_at N90238 2712 EST 3.13 up 0.02492
 rc_N91773_at N91773 2719 lysyl oxidase 4.31 up 0.00302
 rc_N92948_s_at N92948 2726 nuclear phosphoprotein similar to *S. cerevisiae* PWP1 4.09 up 0.0019
 rc_N93299_f_at N93299 2732 nuclear receptor co-repressor 1 6.99 up 0.0371
 rc_N93316_at N93316 2733 EST 3.16 up 0.01262
 rc_N798_at N93798 2738 protei tyrosine phosphatase type IVA, member 3 4.91 up 0.00245
 rc_N98464_s_at N98464 2744 EST 3.68 up 0.03007
 rc_N98758_f_at N98758 2745 EST 3.54 up 0.02609
 rc_N99944_s_at N99944 2749 EST 3.46 up 0.00104
 rc_R05316_s_at R05316 2760 EST 4.2 up 0.00011
 rc_R06251_f_at R06251 2764 tumor protein D52-like 2 4.88 up 0.03097
 rc_R06254_f_at R06254 2765 tumor protein D52-like 2 3.53 up 0.04865
 rc_R06400_at R06400 2768 EST 3.03 up 0.03266
 rc_R06986_f_at R06986 2776 peptidylprolyl isomerase B (cyclophilin B) 7.03 up 0.00628
 rc_R07172_i_at R07172 2777 EST 5.54 up 0.01322
 rc_R15740_at R15740 2791 carbohydrate (keratan sulfate Gal-6) sulfotransferase 1 3.36 up 0.00268
 rc_R16144_at R16144 2794 EST 3.24 up 0.0087
 rc_R20817_s_at R20817 2797 ubiquitin-conjugating enzyme E2A (RAD6 homolog) 3.03 up 0.01091
 rc_R22565_at R22565 2800 EST 3.52 up 0.04352 Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_R26744_at R26744 2804 midline 1 (Opitz/BBB syndrome) 3.8 up 0.00266
 myristoylated alanine-rich protieninase C substrate
 rc_R27016_s_at R27016 2806 (MARCKS, 80K-L) 3.53 up 0.03056
 rc_R27296_f_at R27296 2807 EST 3.41 up 0.00309
 UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase,
 rc_R28636_at R28636 2809 polypeptide 3 3.06 up 0.03678
 rc_R31607_at R31607 2813 EST 3.41 up 0.00163
 rc_R33498_s_at R33498 2810 EST 3.5 up 0.0336
 rc_R39191_s_at R39191 2834 KIAA1020 protein 5.18 up 0.03185
 R39390_at R39390 2837 EST 4.18 up 0.0004
 rc_R39610_s_at R39610 2838 calpain, large polypeptide L2 3.13 up 0.01863
 rc_R43952_at R43952 2853 homeo box B5 3.39 up 0.04829
 rc_R44617_f_at R R44617 2857 MyoD family inhibitor 6.54 up 0.02505

rc_R44793_at R44793 2859 EST 5.4 up 0.00329
 rc_R44839_at R44839 2861 i-beta-1,3-N-acetylglucosaminyltransferase 5 up 0.01812
 rc_R454569_at R45569 2864 DKFZP547E1010 protein 3.96 up 0.00259
 rc_R45994_f_at R45994 2867 EST 6.48 up 0.00358
 rc_R46079_f_at R46079 2868 EST 3.03 up 0.00755
 rc_R46337_s_at R46337 2869 secretory carrier membrane protein 3 3.01 up 0.00374
 rc_R48447_at R48447 2871 EST 4.76 up 0.00533
 rc_R48473_f_at R48473 2872 EST 3.46 up 0.01196
 rc_R48594_s_at R48594 2875 EST 6.15 up 0.03831
 rc_R49395_s_at R49395 2881 EST 3.31 up 0.00867
 rc_R49476_at R49476 2883 EST 4.93 up 0.00763
 rc_R49482_at R49482 2884 EST 3.27 up 0.0161
 rc_R49708_s_at R49708 2886 EST 4.56 up 0.03767
 rc_R51908_s_at R51908 2892 EST 3.16 up 0.0083
 rc_R52161_at R52161 2893 EST 3.41 up 0.00053
 rc_R52649_at R52649 2894 EST 4.69 up 0.00135
 rc_R53109_f_at R53109 2899 dimethylarginine dimethylaminohydrolase 2 3.31 up 0.02406
 rc_R54614_s_at R54614 2902 EST 3.22 up 0.00334 Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_R56095_s_at R56095 2906 EST 3.67 up 0.0158
 rc_R60512_s_at R60512 2918 KIAA0191 protein 3.08 up 0.00856
 rc_R61374_at R61374 2921 EST 4.33 up 0.01489
 rc_R61557_at R61557 2922 KIAA0100 gene product 3.9 up 0.00292
 rc_R62456_at R62456 2925 EST 3.44 up 0.00285
 rc_R66469_f_at R66469 2937 pleckstrin and Sec7 domain protein 3.52 up 0.0272
 rc_R70005_at R70005 2944 EST 4.98 up 0.00007
 rc_R70253_at R70253 2945 EST 3.38 up 0.03125
 rc_R70532_at R70532 2947 EST 3.44 up 0.02186
 rc_R70801_s_at R70801 2950 EST 6.06 up 0.00291
 rc_R71395_at R71395 2952 EST 4.12 up 0.03719
 rc_R72886_s_at R72886 2956 KIAA0422 protein 5.5 up 0.00091
 rc_R73569_s_at R73569 2960 EST 3.54 up 0.01962
 O-linked N-acetylglucosamine (GlcNAc) transferase
 (UDP-N-acetylglucosamine:polypeptide-N-
 rc_R76782_s_at R76782 2963 acetylglucosaminyl transferase) 3.73 up 0.00094
 rc_R77451_i_at R77451 2964 EST 3.67 up 0.00078
 rc_R79246_f_at R79246 2969 melanoma adhesion molecule 6.06 up 0.00057
 rc_R91753_at R91753 2983 EST 3.45 up 0.02391
 rc_R91819_at R91819 2984 EST 12.81 up 0.00037
 rc_R92449_s_at R92449 2985 KIAA0323 protein 4.34 up 0.00104
 rc_R96527_s_at R96527 2999 KIAA0253 protein 4.62 up 0.00702
 rc_R96924_s_at R96924 3001 EST 7.04 up 0.00012
 S67070_at S67070 3023 heat shock 27kD protein 2 3.12 up 0.01688
 S78187_at S78187 3036 cell division cycle 25B 4.83 up 0.00547
 rc_T03438_s_at T03438 3043 EST 3.79 up 0.02042
 rc_T03580_f_at T03580 3046 pyruvate kinase, muscle 5.57 up 0.01344
 rc_T03749_at T03749 3048 KIAA1089 protein 4.23 up 0.00776
 rc_T10316_s_at T10316 3052 EST 3.2 up 0.04794
 rc_T10698_s_at T10698 3054 EST 3.86 up 0.00195
 rc_T15852_f_at T15852 3062 EST 5.21 up 0.00642 Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_T16206_s_at T16206 3065 EST 4.29 up 0.00868
 rc_T16226_at T16226 3066 EST 7.23 up 0.00119
 rc_T16550_at T16550 3072 vacuolar protein sorting 45B (yeast homolog) 5.88 up 0.00004
 rc_T16652_s_at T16652 3073 BCS1 (yeast homolog)-like 3.63 up 0.00434
 rc_T16983_s_at T16983 3074 cleavage and polyadenylation specific factor 4, 30kD 4.23 up 0.0106
 rc_T17066_s_at T17066 3075 SET domain, bifurcated, 1 5.14 up 0.00073
 rc_T17339_f_at T17339 3076 EST 3.29 up 0.00669
 rc_T17353_s_at T17353 3077 EST 3.52 up 0.02085
 rc_TV2326_s_at T23426 3079 EST 3.51 up 0.00674
 rc_T23465_at T23465 3081 EST 3.64 up 0.00265
 rc_T23516_f_at T23516 3083 3-phosphoglycerate dehydrogenase 3.39 up 0.00551
 rc_T24068_s_at T24068 3088 EST 8.65 up 0.00118
 rc_T26471_at T26471 3094 EST 3.76 up 0.0165
 X-ray repair complementing defective repair in Chinese
 rc_T26646_f_at T26646 3097 hamster cells 1 3.49 up 0.02482
 rc_T30214_at T30214 3099 EST 4.46 up 0.03654
 rc_T33489_s_at T33489 3105 EST 4.6 up 0.00285
 rc_T33508_s_at T33508 3106 phosphatidylinositol-4-phosphate 5-kinase, type II, beta 4.96 up 0.00064
 rc_T33619_s_at T33619 3107 EST 3.36 up 0.01283
 rc_T33625_at T33625 3108 EST 3.36 up 0.04096
 rc_T33859_at T33859 3109 KIAA0365 gene product 3.9 up 0.0019
 potassium voltage-gated channel, shaker-related
 T34377_at T34377 3111 subfamily, beta member 2 4.55 up

0.00041
 rc_T40439_s_at T40439 3115 small nuclear ribonucleoprotein polypeptide B" 3.06 up
0.02842
 rc_T41078_at T41078 3121 bromodomain adjacent to zinc finger domain, 2B 3.08 up
0.03426
 rc_T47032_s_at T47032 3124 partner of RAC1 (arfaptin 2) 6.09 up 0.00019

rc_T47325_s_at T47325 3125 EST 5.6 up 0.02923
 ceroid-lipofuscinosis, neuronal 3, juvenile
(Batten,
 rc_T47969_s_at T47969 3128 Spielmeier-Vogt disease) 3.19 up 0.02283

rc_T51972_at T51972 3140 EST 3.44 up 0.00406 Table 7B. Down regulated in hepatocellular
carcinoma versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold
Change Direction Pvalue
 cytochrome P450, subfamily XIA (cholesterol side chain

rc_T53590_s_at T53590 3144 cleavage) 5.09 up 0.00002
 rc_T55196_at T55196 3147 EST 4.24
up 0.00046
 rc_T58607_at T58607 3155 EST 6.83 up 0.03711
 rc_T59668_s_at T59668
3160 lysyl oxidase 3.5 up 0.00083
 rc_T62521_at T62521 3168 EST 4.1 up 0.00392

rc_T62918_at T62918 3169 EST 5.25 up 0.00687
 rc_T65957_f_at T65957 3176 ribosomal
protein S3A 3.94 up 0.04187
 rc_T66935_at T66935 3179 EST 3.01 up 0.00123

rc_T67053_f_at T67053 3180 EST 5 up 0.01846
 rc_T77733_s_at T77733 3219 tubulin, gamma 1
4 up 0.00526
 rc_T78922_s_at T78922 3222 stem cell growth factor; lymphocyte secreted C-type
3.89 up 0.00604
 rc_T79477_s_at T79477 3223 death-associated protein 6 4.4 up 0.00074

rc_T831393_s_at T831393 3228 HMT1 (hnRNP methyltransferase, C. cerevisiae)-like 1 3.32 up
0.0023
 rc_T88814_at T88814 3242 EST 4.87 up 0.00001
 rc_T89703_at T89703 3244 EST
5.27 up 0.00019
 rc_T90190_s_at T90190 3247 H1 histone family, member 2 4.88 up
0.00555
 rc_T94452_at T94452 3257 EST 3.23 up 0.02245
 rc_T95057_f_at T95057 3259
EST 6.46 up 0.00613
 rc_T97679_at T97679 3266 EST 3.32 up 0.01566
 rc_T99312_at
T99312 3270 EST 3.22 up 0.00084
 U18018_at U18018 3317 ets variant gene 4 (E1A enhancer-
binding protein, E1AF) 3.9 up 0.0403
 U18321_at U18321 3318 death associated protein 3 3.14 up
0.00833
 proteasome (prosome, macropain) 26S subunit, non-
 U24704_at U24704 3332
ATPase, 4 3.45 up 0.00037
 cyclin-dependent kinase inhibitor 2A melanoma, p16,

U26727_at U26727 3337 inhibits CDK4) 3.53 up 0.02913
 U30825_at U30825 3343 splicing
factor, arginine/serine-rich 9 3.07 up 0.01928
 U45285_at U45285 3364 T-cell, immune regulator
1 5.75 up 0.00006
 U47025_s_at U47025 3368 phosphorylase, glycogen; brain 4.47 up 0.00037
Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.
 <P>Affy ID
Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 siaH binding protein 1; FBP
interacting repressor;
 pyrimidine tract binding splicing factor; Ro
 U51586_at U51586 3386
ribonucleoprotein-binding protein 1 3.65 up 0.00403
 gamma-glutamyl hydrolase
(conjugase,
 U55206_at U55206 3392 folylpolyglutaminyl hydrolase) 3.34 up 0.00315

U59321_at U59321 3398 DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 17 3.12 up 0.02469

U62392_at U62392 3403 zinc finger protein 193 3.56 up 0.0407
 U66661_at U66661 3406
gamma-aminobutyric acid (GABA) A receptor, epsilon 3.55 up 0.0045
 U68142_at U68142 3411
RAB2, member RAS oncogene family-like 3.02 up 0.0296
 SHC (Src homology 2 domain-
containing) transforming
 U73377_at U73377 3417 protein 1 4.64 up 0.00081
 U73379_at
U73379 3418 ubiquitin carrier protein E2-C 3.32 up 0.00808
 U75285_rna1_at U75285 3422
apoptosis inhibitor 4 (survivin) 5.32 up 0.01127
 U85625_at U85625 3448 ribonuclease 6
precursor 4 up 0.01664
 U90426_at U90426 3453 nuclear RNA helicase, DECD variant of DEAD
box family 3.24 up 0.00035
 U90551_at U90551 3457 H2A histone family, member L 3.54 up
0.01523
 U90904_at U90904 3458 EST 3.02 up 0.00381
 U91930_at U91930 3460 adaptor-
related protein complex 3, delta 1 subunit 3.68 up 0.00009
 rc_W02041_at W02041 3466 EST
5.34 up 0.00027
 rc_W02695_at W02695 3437 EST 3.1 up 0.04745
 rc_W04507_s_at
W04507 3469 prefoldin 4 3.02 up 0.04091
 rc_W04550_at W04550 3470 EST 4.01 up
0.00349
 rc_W15495_at W15495 3474 chromosome 21 open reading frame 5 3.09 up
0.00491
 W26716_at W26716 3482 non-histone chromosome protein 2 (S. cerevisiae)-like 1 5.47
up 0.00146
 W28362_at W28362 3488 KIAA0974 protein 4.38 up 0.00322
 W28366_at
W28366 3489 EST 3.21 up 0.01007
 rc_W31906_at W31906 3497 secretogogin 6.62 up
0.00926
 rc_W42627_f_at W42627 3511 EST 4.37 up 0.00021
 rc_W42674_at W42674

3512 EST 3.07 up 0.0261
 rc_W42778_at W42778 3513 EST 3.27 up 0.02411
 rc_W42788_at W42788 3514 deoxynucleotidyltransferase, terminal 3.24 up 0.02261 Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 rc_W42957_at W42957 3516 calmodulin 2 (phosphorylase kinase, delta) 5.79 up 0.03669
 rc_W44557_at W44557 3518 chromosome 1 open reading frame 4.1 up 0.00433
 rc_W45320_f_at W45320 3523 KRAB-associated protein 1 10.05 up 0.00002
 rc_W46286_s_at W46286 3526 EST 3.68 up 0.00311
 rc_W46634_at W46634 3530 EST 5.03 up 0.02152
 rc_W46810_s_at W46810 3531 HMT1 (hnRNP methyltransferase, S. cerevisiae)-like 2 3.17 up 0.03434
 rc_W46846_at W46846 3532 EST 5.11 up 0.00025
 rc_W46947_at W46947 3533 EST 3.42 up 0.04665
 rc_W47206_at W47206 3535 EST 3.23 up 0.01931
 W49743_at W49743 3540 EST 3.11 up 0.01121
 rc_W49791_at W49791 3541 plasminogen activator, tissue 3.58 up 0.02438
 rc_W56642_at W56642 3547 EST 3.15 up 0.00654
 rc_W57931_at W57931 3549 EST 3.01 up 0.02661
 rc_W58081_a W58081 3550 neuroendocrine-specific protein C like (foocen) 3.05 up 0.03767
 W58247_s_at W58247 3551 kinesin family member 4 3.08 up 0.00048
 DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide, Y
 rc_W60097_at W60097 3556 chromosome 4.82 up 0.04903
 rc_W60486_at W60486 3558 EST 4.27 up 0.0046
 rc_W63608_at W63608 3564 EST 3.33 up 0.02443
 W69302_at W69302 3573 EST 4.37 up 0.00165
 rc_W69468_at W69468 3574 EST 3.25 up 0.00055
 rc_W70336_at W70336 3579 EST 4.46 up 0.00023
 rc_W72187_at W72187 3582 EST 3.09 up 0.00134
 rc_W72276_at W72276 3583 EST 3.56 up 0.0476
 rc_W73038_at W73038 3588 EST 4.83 up 0.00902
 rc_W74536_s_at W74536 3598 advanced glycosylation end product-specific receptor 3.07 up 0.00251
 rc_W78057_at W78057 3600 EST 5.53 up 0.01231
 rc_W79421_at W79421 3603 EST 3.57 up 0.00895
 rc_W79773_at W79773 3605 EST 4.89 up 0.00034
 rc_W80730_at W80730 3607 EST 3.35 up 0.01526
 rc_W80763_at W80763 3608 EST 4.98 up 0.01026 Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein
 rc_W80852_at W80852 3609 retention recepto 3 6.37 up 0.00005
 rc_W81654_at W81654 3616 SRY (sex determining region Y)-box 13 6.06 up 0.00127
 rc_W84447_at W84447 3617 EST 3.34 up 0.00986
 rc_W85875_at W85875 3620 EST 4.91 up 0.01198
 rc_W86214_at W86214 3625 EST 4.3 up 0.00194
 rc_W86748_at W86748 3629 EST 5.09 up 0.01182
 rc_W90146_f_at W90146 3644 EST 3.58 up 0.00322
 rc_W92608_s_at W92608 3653 BAI1-associated protein 3 4.84 up 0.00599
 rc_W94281_s_at W94281 3658 integral membrane protein 2C 3.51 up 0.01689
 rc_W94885_at W94885 3660 EST 6.53 up 0
 rc_W95841_at W95841 3666 EST 3 up 0.00466
 X04347_s_at X04347 3680 heterogeneous nuclear ribonucleoprotein A1 3.34 up 0.00123
 X05610_at X05610 3685 collagen, type IV, alpha 2 6.04 up 0.00062
 collagen, type III, alpha 1 (Ehlers-Danlos syndrome type
 X06700_s_at X06700 3688 IV, autosomal dominant) 3.58 up 0.02964
 keratin 10 (dpidemiolytic hyperkeratosis; keratosis
 X14487_rna1_s_at X14487 3702 palmaris et plantaris) 3.19 up 0.01268
 X14850_at X14850 3706 H2A histone family, member X 3.13 up 0.01523
 X17567_s_at X17567 3719 small nuclear ribonucleoprotein polypeptides B and B1 3.96 up 0.00317
 X53331_at X53331 3727 matrix Gla protein 3.95 up 0.0151
 X54667_s_at X54667 3731 cystatin S, cystatin SN 3.51 up 0.00187
 X54941_at X54941 3728 CDC28 protein kinase 1 3.99 up 0.0016
 X54942_at X54942 3733 CD28 protein kinase 2 3.8 up 0.0035
 X56494_at X56494 3738 pyruvate kinase, muscle 3.65 up 0.04795
 X57129_at X57129 3743 H1 histone family, member 2 4.63 up 0.00663
 X57809_s_at X57809 3746 immunoglobulin lambda locus 3.64 up 0.02655
 X62153_s_at X62153 3754 minichromosome maintenance deficient (S. cerevisiae) 3 3.44 up 0.00704
 X62534_s_at X62534 3755 high-mobility group (nonhistone chromosomal) protein 2 3.39 up 0.0186
 X64364_at X64364 3764 basigin 3.57 up 0.00902
 X66899_at X66899 3772 Ewing sarcoma breakpoint region 1 3.41 up 0.03777 Table 7B. Down regulated in hepatocellular carcinoma versus normal sample set 2.
 <P>Affy ID Genbank Seq ID Known Gene Name Fold Change Direction Pvalue
 transmembrane protein (63kD),

endoplasmic
 X69910_at X69910 3787 reticulum/Golgi intermediate compartment 3.35 up
 0.00898
 X74801_at X74801 3791 chaperonin containing TCP1, subunit 3 (gamma) 3.86 up
 0.00453
 X79563_at X79563 3804 heterogeneous nuclear ribonucleoprotein A1 3.06 up
 0.00449
 X83425_at X83425 3812 Lutheran blood group (Auburger b antigen included) 3.66 up
 0.02661
 X87212_at X87212 3816 cathepsin C 3.45 up 0.02486
 DNA segment on
 chromosome X (unique) 9879
 X92896_at X92896 3829 expressed sequence 3.1 up 0.0405

 X99920_at X99920 3843 S100 calcium-binding protein A13 4.66 up 0.00113
 Y00705_at Y00705
 3850 serine protease inhibitor, Kazal type 1 28.88 up 0.00003
 Y00764_at Y00764 3851
 ubiquinol-cytochrome c reductase hinge protein 3.04 up 0.01294
 Y08302_at Y08302 3852 dual
 specificity phosphatase 9 3.48 up 0.00787
 Y08999_at Y08999 3855 actin related protein 2/3
 complex, subunit 1A (41 kD) 3.13 up 0.02376
 eukaryotic translation elongation factor 1 delta
 (guanine
 Z21507_at Z21507 3867 nucleotide exchange protein) 3.57 up 0.01898

 Z23090_at Z23090 3868 heat shock 27kD protein 1 3.69 up 0.00628
 Z24727_at Z24727 3871
 tropomyosin 1 (alpha) 3.64 up 0.00388
 Z37987_s_at 3797 3882 glypican 3 10.66 up
 0.02304
 rc_Z38299_at Z38299 3887 EST 3.71 up 0.0036
 rc_Z38431_at Z38431 3889 EST
 3.09 up 0.0083
 rc_Z38444_at Z38444 3891 KIAA0923 protein 3.38 up 0.02918

 rc_Z38462_at z38462 3982 k1aa0938 PROTEIN 4.69 UP 0.0142
 rc_Z38904_at Z38904 3896 EST
 3.02 up 0.00814
 rc_Z389191_at z39191 3901 EST 3.47 up 0.00756
 rc_Z39200_at Z39200
 3902 EST 4.07 up 0.00075
 rc_Z39379_at Z39379 3903 EST 3.77 up 0.00513
 rc_Z39429_at
 Z39429 3906 EST 3.58 up 0.00416
 rc_Z39682_s_at Z39682 3911 KIAA0954 protein 6.96 up
 0.01966
 rc_Z40006_at Z40006 3917 EST 3.54 up 0.00156
 rc_Z40883_r_at Z40883 3924
 EST 3.26 up 0.01863
 rc_Z41349_at Z41349 3931 EST 3.45 up 0.01503 Table 7B. Down
 regulated in hepatocellular carcinoma versus normal sample set 2.
 <P>Affy ID Genbank Seq ID
 Known Gene Name Fold Change Direction Pvalue
 succinate dehydrogenase complex, subunit
 A,
 rc_Z41747_at Z41747 3936 flavoprotein (Fp) 3.04 up 0.01336
 Z47727_at Z47727 3940
 polymerase (RNA) II (DNA directed) polypeptide K 3.28 up 0.00317
 Z74615_at Z74615 3949
 collagen, type I, alpha 1 5.47 up 0.00283
 Z74616_s_at Z74616 3950 collagen, type I, alpha 2 5.95
 up 0.02212 Table 8A. Genes and ESTs expressed only in hepatocellular carcinoma versus normal
 sample set 2.
 fold hcc hcc hcc
 change sample sample sample normal normal normal
 in
 hcc set 2: set 2: set 2: set 2: set 2: set 2:
 Affy ID Genbank Seq ID Known Gene Name set 2 p
 value Mean Median Std Dev Mean Median Std Dev
 DEK oncogene (DNA
 AA093497_s_at
 AA093497 199 binding) #N/A #N/A 180.58 107.64 165.71 52.11 48.84 26.51

 AA248283_at AA248283 534 EST #N/A #N/A 67.18 45.86 55.18 21.63 18.96 11.71

 AA291456_s_at AA291456 700 EST #N/A #N/A 828.34 830.24 196.63 671.21 509.58
 629.13
 GAS2-related on
 AA400643_s_at AA400643 817 chromosome 22 4.04 0.03751
 118.72 123.18 137.15 -43.6 -33.96 60.39
 AA420179_at AA420179 930 EST #N/A
 #N/A 37.17 34.26 18.5 15.27 16.75 15.28
 Notch (Drosophila) homolog

 AA428172_f_at AA428172 986 3 9.68 0.00195 335.57 374.9 231.52 -9.64 -15.61 56.16

 AA464043_s_at AA464043 1255 EST 3.99 0.00056 116.97 115.99 53.49 14.27 10.06 25.86

 H19562_at H19562 1896 PTD010 protein #N/A #N/A 522.13 432.65 256.94 393.61 326.53
 182.71
 L08044_s_at L08044 2149 trefoil factor 3 (intestinal) #N/A #N/A 214.6
 108.17 238.79 107.82 58.55 184.16
 L29218_s_at L29218 2190 CDC-like kinase 2 6.51 0.00019
 219.64 237.35 104.29 6.53 -10.03 59.8
 L37747_s_at L37747 2206 lamin B1 #N/A
 #N/A 43.42 28.65 37.33 5.97 5.1 7.57
 N34257_at N34257 2495 EST #N/A
 #N/A 20.76 21.48 19.54 -1.84 -2.74 8.53
 R50692_at R50692 2888 KIAA0476 gene
 proeduct #N/A #N/A 197.89 187.87 101.08 148.53 151.12 63.03
 R60368_at R60368
 2917 EST #N/A #N/A 29.68 28.93 31.9 -28.29 -26.44 41.68
 R66475_at R66475 2938
 EST #N/A #N/A 45.68 32.34 34.37 7.64 8.26 6.3
 potassium voltage-gated

 channel, shaker-related
 T34377_at T34377 3111 subfamily, beta member 2 4.55 0.00041 113.59
 120.58 51.65 6.87 11.17 25.69
 DEAD/H (Asp-Glu-Ala-
 Asp/His) box polypeptide 11

 (S.cerevisiae CHL1-like
 V75968_s_at U75968 3423 helicase) #N/A #N/A 187.33

200.16 90.35 115.5 102.24 77.72
 W21426_at W21426 381 KIAA0806 gene product #N/A
#N/A 63.36 64.93 20.23 45.59 40.39 19.89
 W28696_i_at W28696 3491 EST #N/A
#N/A 14.7 20.64 17.12 4.28 4.33 2.47 Table 8A. Genes and ESTs expressed only in hepatocellular
carcinoma versus normal sample set 2.
 fold hcc hcc hcc
 change sample sample sample
normal normal normal
 in hcc set 2: set 2: set 2: set 2: set 2: set 2:
 Affy ID Genbank Seq ID
Known Gene Name set 2 p value Mean Median Std Dev Mean Median Std Dev
 H1 histone
family, member
 X57129_at X57129 3743 2 4.63 0.00663 137.13 137.75 87.31 8.38 5.39
28.3
 rc_AA024658_at AA024658 47 ribosomal protein S19 7.55 0.00592 278.11 120.83 373.3
7.62 5.03 10.68
 rc_AA029288_at AA029288 65 EST 3.36 0.04908 134.53 56.15 209.69 4.09 3.35
8.39
 rc_AA037828_at AA037828 88 KIAA0614 protein #N/A #N/A 53.61 46.86
41.68 13.32 10.65 11.96
 rc_AA040465_at AA040465 95 EST 3.63 0.01806 229.8 210.67 180.94
47.15 45.53 5.48
 rc_AA053660_at AA053660 128 EST #N/A #N/A 543.66 223.47
685.44 95.24 79.97 42.99
 cAMP responsive element
 rc_AA136332_at AA136332 299
binding protein 3 (luman) #N/A #N/A 49.04 33.07 31.07 -18.27 -20.23 13.05

rc_AA149530_at AA149530 324 interferon regulatory factor 3 #N/A #N/A 32.94 23.12
34.23 4.21 5.38 8.53
 rc_AA149586_at AA149586 325 EST #N/A #N/A 24.99 26.6
34.37 5.26 9.11 23.41
 rc_AA206023_at AA206023 427 EST #N/A #N/A 154.13
170.36 85.33 108.57 111.76 58.39
 N-ethylmaleimide-sensitive
 rc_aa234530_s_at
AA234530 484 factor #N/A #N/A 143.67 135.48 82.59 51.33 42.9 35.02

rc_AA251909_at AA251909 549 EST 3.59 0.01129 92.19 79.34 72.73 8.88 11.22 8.27

rc_AA262030_at AA262030 605 EST #N/A #N/A 119.75 89.66 103.84 31.51 32.91
14.46
 ribonuclease HI, large
 rc_AA262477_at AA262477 608 subunit 4.57 0.00724 242.42
199.5 182.26 44.51 36.87 22.37
 rc_AA283759_at AA283759 671 EST #N/A #N/A
91.82 76.73 42.28 46.87 45.86 21.54
 rc_AA291644_at AA291644 701 EST 3.28 0.00033 11473
117.29 44.59 32.77 30.24 21.1
 rc_AA338760_at AA338760 744 EST 3.96 0.01307 129.77 130.26
87.27 14.91 21.91 26.96
 rc_RC398205_at AA398205 789 EST 4.22 0.00059 125.4 107.84 63.85
15.01 7.37 26.26
 tumor suppressor deleted in
 rc_AA401965_at AA401965 833 oral cancer-
related 1 7.58 0.00089 932.74 924.02 593.69 120.58 93.29 109.41
 rc_AA402272_at AA402272
837 EST 3.73 0.02336 348.91 340 230.15 99.7 92.28 80.27
 rc_AA404597_at AA404597 854 EST
#N/A #N/A 609.98 525.02 371.31 379.26 336.33 167.43
 rc_AA417030_at AA417030
914 EST 7.35 0.00555 200.3 168.21 135.63 6.42 7.5 7.77 Table 8A. Genes and ESTs expressed only in
hepatocellular carcinoma versus normal sample set 2.
 fold hcc hcc hcc
 change sample
sample sample normal normal normal
